



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶: C12Q 1/68	A2	(11) International Publication Number: WO 99/51779 (43) International Publication Date: 14 October 1999 (14.10.99)
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(54) Title: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS (57) Abstract Methods and compositions for preventing and treating glaucoma; and glaucoma diagnostics are disclosed.		

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Glaucoma Therapeutics and Diagnostics

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1. Background of the Invention

Glaucoma is an optic nerve disorder characterized by cupping of the optic nerve head and loss of peripheral vision. Occasionally there is also loss of central vision. In the majority of patients, an elevated intraocular pressure is present and is
 10 thought to contribute to the optic nerve damage. Glaucoma is the second leading cause of blindness in developed countries (Leske, M.C. (1983) *Am. J. of Epidemiology* 118:166-191). Its prevalence increases with age and is greater in black patients (Leske, M.C. (1983) *Am. J. of Epidemiology* 118:166-191). Glaucoma affects approximately 2.3 million Americans and blinds approximately 12,000 of them per year (Tielsch, J.M.
 15 (1993) Therapy for glaucoma: costs and consequences. In *Transactions of the New Orleans Academy of Ophthalmologists*, S.F. Ball, Franklin, R.M. (Ed.), pp 61-68. Kugler, Amsterdam).

The most prevalent form of glaucoma is primary open angle glaucoma (POAG), a progressive disease of the optic nerve characterized by degeneration and
 20 cupping of the optic nerve, loss of peripheral visual field, and increased intra-ocular pressure. Evidence indicates that POAG is genetically heterogeneous with a complex mode of inheritance. An early onset form of POAG known as juvenile open angle glaucoma (JOAG) is an autosomal dominant disorder with high penetrance.

A significant fraction of glaucoma has a genetic basis (Benedict, T.W.G.
 25 Abhandlungen aus dem Gebiete der Augenheilkunde. Breslau: L. Freunde (1842); Stokes, (1940) *W. Arch Ophthalmol* 24:885-909; Kellerman, L. and A. Posner, (1955) *Am. J. Ophthalmol.* ;40:681-685; Becker, B., et al., (1960) *Am. J. Ophthalmol.* 50:557-567; Francois, J., et. al., (1966) *Am. J. Ophthalmol.*;62:1067-1071; Armaly, M.F. (1967) *Arch Ophthalmol*;78:35-43; Davies, T.G.. (1968) *Br. J. Ophthalmol.*:52:31-39; Jay, B.,
 30 Paterson, G. (1970) *Trans. Ophthalmol. Soc. U.K.*;90:161-171; Paterson, G. (1970) *Trans. Ophthalmol. Soc. U.K.*;90:515-525; Miller, S.J.H. (1978) *Trans. Ophthalmol. Soc. U.K.* 98:290-292), which allows genetic methods to be used to investigate the pathophysiological mechanisms of the disease at the molecular level. The chromosomal locations of genes causing three genetically distinct types of primary open angle
 35 glaucoma have been identified (Sheffield, V., et al. (1993) *Nature Genetics* 4:47-50;

Sunden, S.L.F., *et al.* (1996) 6:862-869; Richards, J.E., *et al.* (1994) *Am. J. Hum. Genet.*:54:62-70; Wiggs, J.L., *et al.* (1994) *Genomics*:21:299-303; Stoilova, D., *et al.* (1996) *Genomics* 36:142-150; Wirtz, M.K., *et al.* (1997) *Am. J. Hum. Genet.* 60:296-304).

Therapeutics, which modulate (agonize or antagonize) genes (wild-type or mutant) involved in glaucoma, would be useful for the prevention and treatment of glaucoma. In addition, the detection of mutations in genes that correlate with the existence or a predisposition to the development of glaucoma can provide useful diagnostics.

2. Summary of the Invention

In one aspect, the invention features isolated GLC1A nucleic acid molecules. The disclosed molecules can be non-coding, (e.g. probe, antisense or ribozyme molecules) or can encode a functional polypeptide (e.g. a polypeptide which specifically modulates, e.g., by acting as either an agonist or antagonist, at least one bioactivity of a myocilin polypeptide).

In further embodiments, the nucleic acid molecule is a GLC1A nucleic acid that is at least 70%, preferably 80%, more preferably 85%, and even more preferably at least 95% homologous in sequence to the nucleic acids shown as SEQ ID No. 7 or 9 or to the complement thereof. In another embodiment, the nucleic acid molecule encodes a polypeptide that is at least 92% and more preferably at least 95% similar in sequence to the polypeptide shown in SEQ ID No: 8 or 10.

The invention also provides probes and primers comprising substantially purified oligonucleotides, which correspond to a region of nucleotide sequence which hybridizes to at least about 6 consecutive nucleotides of the sequences set forth as SEQ ID Nos: 1, 2, 3, 4, 5 or 6 or complements of the sequences set forth as SEQ ID Nos: 1, 2, 3, 4, 5 or 6 or naturally occurring mutants thereof. In preferred embodiments, the probe/primer further includes a label group attached thereto, which is capable of being detected.

For expression, the subject GLC1A nucleic acids can include a transcriptional regulatory sequence, e.g. at least one of a transcriptional promoter (e.g., for constitutive expression or inducible expression) or transcriptional enhancer or suppressor sequence, which regulatory sequence is operably linked to the GLC1A gene sequence. Such regulatory sequences in conjunction with a GLC1A nucleic acid

molecule can provide a useful vector for gene expression. This invention also describes host cells transfected with said expression vector whether prokaryotic or eukaryotic and *in vitro* (e.g. cell culture) and *in vivo* (e.g. transgenic) methods for producing GLC1A proteins by employing said expression vectors.

5 In another aspect, the invention features isolated myocilin polypeptides, preferably substantially pure preparations, e.g. of plasma purified or recombinantly produced myocilin polypeptides. In one embodiment, the polypeptide is identical to or similar to a myocilin protein represented in SEQ ID No: 8 or 10. Related members of the vertebrate and particularly the mammalian myocilin family are also within the scope
10 of the invention. Preferably, a myocilin polypeptide has an amino acid sequence at least about 92% homologous and preferably at least about 95%, 96%, 97%, 98% or 99% homologous to the polypeptide represented in SEQ ID No: 8 or 10. In a preferred embodiment, the myocilin polypeptide is encoded by a nucleic acid which hybridizes with a nucleic acid sequence represented in one of SEQ ID No: 7 or 9. The subject
15 myocilin proteins also include modified proteins, which are resistant to post-translational modification, as for example, due to mutations which alter modification sites (such as tyrosine, threonine, serine or asparagine residues), or which prevent glycosylation of the protein, or which prevent interaction of the protein with intracellular proteins involved in signal transduction.

20 The myocilin polypeptide can comprise a full length protein, such as represented in SEQ ID No: 8 or 10, or it can comprise a fragment corresponding to one or more particular motifs/domains, or to arbitrary sizes, e.g., at least 5, 10, 25, 50, 100, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 460, 470, 475, 480, 485, or 490 amino acids in length.

25 Another aspect of the invention features chimeric molecules (e.g. fusion proteins) comprised of a myocilin protein. For instance, the myocilin protein can be provided as a recombinant fusion protein which includes a second polypeptide portion, e.g., a second polypeptide having an amino acid sequence unrelated (heterologous) to the myocilin polypeptide (e.g. the second polypeptide portion is glutathione-S-
30 transferase, an enzymatic activity such as alkaline phosphatase or an epitope tag).

Yet another aspect of the present invention concerns an immunogen comprising a myocilin polypeptide in an immunogenic preparation, the immunogen being capable of eliciting an immune response specific for a myocilin polypeptide; e.g. a humoral response, an antibody response and/or cellular response. In preferred

embodiments, the immunogen comprises an antigenic determinant, e.g. a unique determinant, from the protein represented in SEQ ID Nos: 8 or 10.

5 A still further aspect of the present invention features antibodies and antibody preparations specifically reactive with an epitope of the myocilin protein. In preferred embodiments the antibody specifically binds to at least one epitope represented in SEQ ID Nos: 8 or 10.

10 The invention also features transgenic non-human animals which include (and preferably express) a heterologous form of a GLC1A gene described herein, or which misexpress an endogenous GLC1A gene (e.g., an animal in which expression of one or more of the subject GLC1A proteins is disrupted). Such a transgenic animal can serve as an animal model for studying cellular and tissue disorders comprising mutated or mis-expressed GLC1A alleles or for use in drug screening. Alternatively, such a transgenic animal can be useful for expressing recombinant myocilin polypeptides.

15 In yet another aspect, the invention provides assays, e.g., for screening test compounds to identify inhibitors, or alternatively, potentiators, of an interaction between a myocilin protein and, for example, a virus, an extracellular ligand of the myocilin protein, or an intracellular protein which binds to the myocilin protein.

20 A further aspect of the present invention provides a method of determining if a subject is at risk for glaucoma or another disorder resulting from a mutant GLC1A gene. The method includes detecting, in a tissue of the subject, the presence or absence of a genetic lesion characterized by at least one of (i) a mutation of a gene encoding a myocilin protein, (e.g., a gene represented in one of SEQ ID Nos: 7 or 9, or a homolog thereof or a mutation of a GLC1A intronic sequence, e.g. as represented in SEQ ID Nos. 1-6); or (ii) the mis-expression of a GLC1A gene. In preferred
25 embodiments, detecting the genetic lesion includes ascertaining the existence of at least one of: a deletion of one or more nucleotides from a GLC1A gene; an addition of one or more nucleotides to the gene, a substitution of one or more nucleotides of the gene, a gross chromosomal rearrangement of the gene; an alteration in the level of a messenger RNA transcript of the gene (e.g., due to a promoter mutation); the presence of a non-
30 wild type splicing pattern of a messenger RNA transcript of the gene; a non-wild type level of the protein; and/or an aberrant level of soluble myocilin protein.

For example, detecting the genetic lesion can include (i) providing a probe/primer comprised of an oligonucleotide which hybridizes to a sense or antisense sequence of a GLC1A gene or naturally occurring mutants thereof, or intronic flanking

sequences naturally associated with the GLC1A gene; (ii) contacting the probe/primer to an appropriate nucleic acid containing sample; and (iii) detecting, by hybridization of the probe/primer to the nucleic acid, the presence or absence of the genetic lesion; e.g. wherein detecting the lesion comprises utilizing the probe/primer to determine the nucleotide sequence of the GLC1A gene and, optionally, of the flanking nucleic acid sequences. For instance, the primer can be employed in a polymerase chain reaction (PCR) or in a ligation chain reaction (LCR). In alternate embodiments, the level of a GLC1A protein is detected in an immunoassay using an antibody which is specifically immunoreactive with the myocilin protein.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

3. Brief Description of the Figures

Figure 1 is an alignment of human and mouse GLC1A gene sequences. The three exons of the human and mouse GLC1A genes and flanking sequences are aligned in panels A, B and C. These sequences are not continuous. Exon sequences are reported in capital letters while flanking sequences are in lower-case letters. Nucleotides conserved between mouse and human are indicated by a closed circle. In panel 1A, exon 1 and flanking promoter and intron 1 sequences are shown. A subset of putative promoter and enhancer elements are underlined and labeled. GRE half-sites are indicated by "GR". A (CA) repeat polymorphism in the 5' flanking region of the human GLC1A gene is also underlined and labeled "(CA) repeat polymorphism". In panel 1B, exon 2 and flanking intron 1 and intron 2 sequences are shown. In panel 1C, exon 3 and flanking intron 2 and downstream sequences are shown. Polyadenylation signal sequences are underlined and labeled "poly-A". A (CA) repeat polymorphism downstream of the human GLC1A gene is also underlined and labeled "(CA) repeat polymorphism".

Figure 2 is a schematic representation of putative motifs that are conserved between human and mouse myocilin proteins.

Figure 3 is an alignment of the proteins predicted by the mouse and human GLC1A genes. Amino acids conserved between mouse and human are indicated by a closed circle. The location of disease-causing mutations previously identified in the human GLC1A gene are indicated. For each missense mutation, the mutant residue is shown directly above the wild-type amino acid. The location of a nonsense mutation is indicated by a "1" and the location of an insertion mutation is indicated by a "2".

4. Detailed Description of the Invention

4.1. General

5 As reported herein, a genetic locus associated with JOAG was identified on chromosome 1q21-q31 by genetic linkage analysis. Observed recombinations between the glaucoma phenotype and highly polymorphic genetic markers in two large JOAG kindreds allowed the interval containing GLC1A gene to be narrowed to a 3 cM region of chromosome 1q between markers D1S3665 and D1S3664. Further evaluation
10 of marker haplotypes revealed that each of three pairs of glaucoma families shared alleles of the same eight contiguous markers suggesting that the GLC1A gene lies within a narrower interval defined by D1S1619 and D1S3664.

Several genes mapping to the GLC1A region of chromosome 1 were considered as candidates for the disease-causing gene. Three genes (LAMC1 (H.C. Watkins et. al., (1993) *Hum. Mol. Genet.* 2: 1084), NPRI (D.G. Lowe et al., (1990) *Genomics* 8:304), and CNR2 (S. Munro et al., (1993) *Nature* 365:61), were excluded from the candidate region by genetic linkage analysis using intragenic polymorphic markers. Five additional candidate genes were determined to lie within the observed recombinant interval by YAC STS content mapping: selectin E (M.P. Bevilacqua et al.,
20 (1989) *Science* 243:1160) (GenBank accession no. M24736); selectin L (T.F. Tedder et al., (1989) *J. Exp. Med.* 170:123) (GenBank accession no. M25280); TXGP-1 (S. Miura et al., (1991) *Mol. Cell Biol* 11:1313) (GenBank accession no. MD90224; APT1LG1 (T. Takahashi et al., (1994) *Int. Immunol.* 6, 1567); and TIGR (Trabecular meshwork Induced Glucocorticoid Response Protein) (J.R. Polansky et al., (1989) *Prog. Clin. Biol. Res* 12:113; J. Escibano et al., (1995) *J. Biochem.* 118:921; *International Patent Application Publication No.* WO 96/14411) (GenBank accession nos. R95491, R95447, R95443, R47209). However, two of these genes (selectin E, and selectin L) were found to lie outside of the shared haplotype interval with this approach. The remaining genes (APT1LG1, TXGP-1, and TIGR) were found to map within the narrowest JOAG
30 interval by both YAC STS content and radiation hybrid mapping.

Two of these genes (APT1LG1 and TIGR) were screened for mutations in families with JOAG. Primers were selected from the available sequence (T. Takahashi et al., (1994) *Int. Immunol.* 6, 1567, J. Escibano et al., (1995) *J. Biochem.* 118:921; *International Patent Application Publication No.* WO 96/14411) (GenBank

accession nos. R95491, R95447, R95443, R47209) and overlapping PCR amplification products were evaluated by single strand conformation polymorphism analysis (B.J. Bassam et al., (1991) *Anal. Biochem.* 196: 80) and direct DNA sequencing. Although the complete cDNA sequence of the APT1LG1 and TIGR genes have been published,
5 the presence of intervening sequences permitted only 85 - 90% of their coding sequences to be screened in genomic DNA. Eight unrelated JOAG patients were screened with the APT1LG1 assay but no sequence variants were identified.

The TIGR gene assay was initially used to screen affected members of four different 1q-linked glaucoma families, and affected members of four smaller
10 families implicated by haplotypic data. Amino-acid-altering mutations were detected in four of eight families. A tyrosine to histidine mutation in codon 437 was detected in all 22 affected members of the original family (V.C. Sheffield et al., (1993) *Nature Genet.* 4:47) linked to 1q. A glycine to valine mutation in codon 364 was detected in two families including one previously unreported adult-onset open angle glaucoma family
15 with 15 affected members. A nonsense mutation (glutamine to stop) at codon 368 was detected in two families. The latter mutation would be expected to result in a truncation of the gene product.

The prevalence of mutations in the two PCR amplimers that harbored these three changes was then estimated by screening four different populations:
20 glaucoma patients with a family history of the disease; unselected primary open angle glaucoma probands seen in a single clinic; the general population (approximated by patients with heritable retinal disease and spouses from families who participated in prior linkage studies); and, unrelated volunteers over the age of 40 with normal intraocular pressures and no personal or family history of glaucoma. PCR products
25 determined to contain a sequence variation by SSCP were sequenced and compared to sequence generated from an unaffected individual as well as the normal chromosome in each affected individual. Overall, missense or nonsense mutations were found in about 3-5% of unrelated glaucoma patients and in about 0.2% of controls. A Chi-square test revealed this difference to be significant ($p < 0.001$).

30 In a subsequent study, SSCP screening followed by sequencing of DNA from 1312 unrelated individuals revealed a total of 33 GLC1A sequence changes. Sequencing of the entire GLC1A coding region amplified from the probands of three families with 1q-linked glaucoma, but without SSCP shifts revealed three additional sequence changes. Sixteen of these 36 sequence variations (Table 1) met the following

criteria for a "probable" disease causing mutation: 1) presence in one or more glaucoma patients; 2) alteration of the predicted amino acid sequence; 3) presence in less than 1% of the general population; 4) absence in the 91 normal volunteers. These sixteen mutations were found in 34 of the 716 glaucoma probands (4.7%). Ten sequence
5 changes failed to alter the predicted amino acid sequence of GLC1A and are therefore likely to be non-disease-causing polymorphisms (Table 3). Nine sequence changes altered the predicted amino acid sequence of GLC1A (eight) or the 5' flanking region (one) but were judged likely to be non-disease-causing polymorphisms (Table 2) for one
10 of the following reasons: they were present in more than 1% of the general population (three), they were found only in the normal or general population (five), or they were found in the same allele as a more likely disease-causing mutation (one).

Table 1
Probable Mutations

5	1) GLN19HIS
	2) ARG82CYS
	3) TRP286ARG
	4) THR293LYS
	5) PRO361SER
	6) GLY364VAL
10	7) GLN368STOP
	8) THR377MET
	9) ASP380GLY
	10) 396INS397
	11) ARG422HIS
15	12) TYR437HIS
	13) ALA445VAL
	14) ARG470CYS
	15) ILE477ASN
	16) LYS500ARG
20	

Table 2
Probable Polymorphism

25	1) GLU352LYS
	2) CYS9SER
	3) ASN73SER
	4) ARG76LYS
	5) LYS398ARG
30	6) ARG422CYS
	7) SER425PRO
	8) TYR473CYS
	9) VAL495ILE7

Table 3
Third Nucleotide (Wobble) Polymorphisms

- 1) PRO13PRO
- 2) GLY122GLY
- 3) LEU159LEU
- 4) LYS266LYS
- 5) THR285THR
- 6) THR325THR
- 7) VAL329VAL
- 8) TYR347TYR
- 9) GLU396GLU
- 10) VAL439VAL

15 Bacterial artificial chromosomes (BACs) containing the human GLC1A gene and its mouse orthologue were subcloned and sequenced to reveal the genomic structure of the genes. Both the human and mouse GLC1A genes are composed of three exons. Human exon 1 (including the 5' promoter region of exon 1, base pairs 1-1905; exon 1, base pairs 1906-2509; and the 5' end of intron 1, base pairs 2510-2800) is set forth as SEQ ID No: 1. Human exon 2 (including the 3' end of intron 1, base pairs 1-193; exon 2, base pairs 194-319; and the 5' end of intron 2, base pairs 320-680) is set forth as SEQ ID No:2. Human exon 3 (including the 3' end of intron 2, base pairs 1-427; exon 3, base pairs 428-1212; and the 3' UTR, base pairs 1213-2000) is set forth as SEQ ID No:3. Mouse exon 1 (including the 5' promoter region of exon 1; base pairs 1-1947; exon 1, base pairs 1948-2509; and the 5' end of intron 1, base pairs 2510-2800) is set forth as SEQ ID No:4. Mouse exon 2 (including the 3' end of intron 1, base pairs 1-193; exon 2, base pairs 194-319; and the 5' end of intron 2, base pairs 320-680) is set forth as SEQ ID No:5 and mouse exon 3 (including the 3' end of intron 2, base pairs 1-427; exon 3, base pairs 428-1212 and the 3' UTR, base pairs 1213-1456) is set forth as SEQ ID No:6. Exons two and three are 126 base pairs and 782 base pairs long in both genes, while exon one is 604 base pairs in the human gene and 562 base pairs in the mouse gene. Exon-intron borders are completely conserved between mouse and human. The human coding GLC1A nucleotide sequence is comprised of 1512 nucleotides (SEQ ID No: 7) and encodes a 504 amino acid myocilin protein (SEQ ID NO. 8) having a molecular weight of about 57kDa. The mouse coding GLC1A nucleotide sequence is

comprised of 1470 nucleotides (SEQ ID No: 9) and encodes a 490 amino acid myocilin protein (SEQ ID No: 10) having a molecular weight of about 55 kDa. The human and mouse coding sequences are 83% identical at the nucleotide level and predict proteins that are 82% identical at the amino acid level.

5 Many putative transcription regulatory sequences were identified in the upstream region of the GLC1A genes (Table 4). Three poly-adenylation sites were located in the 3' UTR of the human gene at positions 1714, 1864 and 2006 base pairs following the putative start codon. Additionally the human GLC1A gene was found to be closely flanked by two CA simple tandem repeat polymorphisms (STRPs) that
10 proved to be useful genetic markers for tracing the segregation of the gene within families.

Table 4
Putative GLC1A promoter and enhancer elements

15	<u>Human and Mouse</u>	<u>Human only</u>	<u>Mouse only</u>
	AP-1	AFP1	DTF-1
	AP-2	CF2-II	GATA-2
	AP-3	CP2	Hb
20	AR	DBP	Lva
	c-ETS	Elk-1	Lvb-binding factor
	c-Myc	G6 Factor	MAF
	C/EBP	HNF-1	MAZ
	CAC-binding protein	HOX-D8	muEBP-C2
25	Dr	HOX-D9	NF-E2
	En	HOX-10	PTFI-beta
	F2F	IRF	TF3-s
	GATA-1	LyF-1	USF
	GFII	MBF-1	
30	GR	MCBF	
	HiNF-A	Myogenin	

	<u>Human and Mouse</u>	<u>Human only</u>
	HNF-3	NF-InsE
	MBF-1	TCF-2alpha
5	MEP-1	TDEF
	NF-1	TGT3
	NF-GMb	TII
	N-Oct-3	UBP-1
	Oct	WT-1
10	PEA3	Pit-1a
	PPAR	
	PR	
	PU.1	
	PuF	
15	Sp1	
	SRY	
	TCF-1A	
	TFIIB	
	TFIIE	
20	TFIIF	
	TMF	
	YY1	
	Zeste	

25

The human GLC1A gene has been placed on the chromosome 1 physical map between four flanking genes (SELL, SELE, GLC1A, APT1LG1, AT3). The mouse homologs of these flanking genes are present in the same order on the mouse chromosome 1, suggesting that the mouse GLC1A gene is located in this syntenic region between the mouse homologues of SELE and APT1LG1.

30

The expression of human GLC1A was examined by Northern blot analysis of RNA from adult tissues. High levels of expression of the 2.3kb mRNA was found in a wide range of tissues including: heart, skeletal muscle, stomach, thyroid, trachea, bone marrow, thymus, prostate, small intestine and colon. Less abundant

GLC1A expression was observed in lung, pancreas, testis, ovary, spinal cord, lymph node and adrenal gland. GLC1A transcripts were not detected in brain, placenta, liver, kidney, spleen or leukocytes. A similar expression pattern was observed in the mouse. To test the possibility that certain regions of the brain were under represented in poly-A
5 selected mRNA of total brain tissue, a Northern blot prepared with RNA from several different regions of the brain were hybridized using a GLC1A probe. Hybridization was observed in the spinal cord, but not in the cerebellum, cerebral cortex, medulla, occipital lobe, frontal lobe, temporal lobe, or putamen.

Figure 2 illustrates protein motifs that are present in both human and
10 mouse GLC1A proteins. Both the GLC1A nucleic acid sequence and encoded myocilin amino acid sequence show homology to nonmuscle myosin in the N-terminal region and to olfactomedin in the C-terminal region. In addition, both human and mouse GLC1A proteins contain a leucine zipper domain similar to that seen in kinectin and other cytoskeletal proteins in the myosin-like domain (spanning amino acids 71-152). This
15 motif consists of two subregions spanning amino acids 71-85 and 103-152 in which leucine residues appear three to eight times at every seventh position. Both the human and the mouse GLC1A nucleic acids include 10 putative phosphorylation sites and 4 putative glycosylation sites. In addition to these functional domains, a hydrophobic domain appears at the N-terminus of the myocilin protein and includes a sequence
20 resembling a signal peptide in which the alanine residue at position 18 may be a possible cleavage site.

Further analysis reveals a hydrophobic region between amino acids 17-37 and 426-44. However, the length and degree of hydrophobicity of these domains suggests that they are not membrane spanning. The carboxy-terminal three amino acids
25 of human GLC1A protein are serine, lysine and methionine. This sequence has been shown to function as a peroxisome targeting sequence in other proteins (Subramani, S (1993) *Ann. Rev. of Cell Bio.* 9:445-478). However, no such putative targeting sequence is present in the mouse protein. Western blot analysis of human GLC1A protein reveals bands at 57 and 59 kD, confirming the predicted protein size and providing evidence that
30 the protein may be glycosylated. These findings suggest that myocilin is a novel cytoskeletal protein involved in the development of neuroepithelium, such as photoreceptor cells.

Figure 3 shows an alignment of the predicted amino acid sequence for the mouse and human GLC1A genes and indicates the position of sixteen mutations with

respect to the mouse and human GLC1A protein sequences. Fourteen of these mutations are missense mutations that result in single amino acid substitutions. Twelve of these occur at amino acids that are conserved between human and mouse while two occur at amino acids that are not conserved. The two remaining mutations include an insertion that disrupts two conserved amino acids and a nonsense mutation that results in the truncation of the terminal 136 amino acids of the GLC1A protein and the loss of 121 conserved residues. Thus, the percentage of disease causing mutations found in amino acids conserved between mouse and human (88%) is not significantly different from the overall protein conservation across species (82%).

Importantly, the GLC1A nucleic acid sequence differs substantially from the TIGR gene sequence reported in International Patent Application No. WO 96/14411 (GenBank accession nos. R95491, R95447, R95443 and R947209). In fact, as reported, the TIGR gene sequence does not encode a functional protein.

A summary of the differences between the GLC1A gene disclosed herein, and the TIGR gene are presented in Table 5.

Table 5
Differences Between GLC1A and TIGR Gene Sequences

1. The "C" at bp #331 of the GLC1A DNA coding sequence is not present in the TIGR sequence.
2. The 29 bps "AGGGGCTGCAGAGGGAGCTGGGCACCCTG" (SEQ ID NO. 11) at bp #344-372 of the GLC1A DNA coding sequence are not included in the TIGR sequence.

Errors 1 and 2 cause the TIGR sequence to wrongly predict 4 amino acids and exclude 10 amino acids from the protein sequence.

3. The "C" at bp #559 of the GLC1A DNA coding sequence is not present in the TIGR sequence.

4. A "T" is wrongly inserted between bp #560 and #561 of the GLC1A DNA coding sequence in the TIGR sequence.

5 Errors 3 and 4 cause the TIGR sequence to incorrectly predict a serine amino acid at residue #187 instead of a glutamine.

- 10 5. The 9 bps "CTCAGGAGT" present at bps 706-714 of the GLC1A DNA coding sequence are wrongly duplicated and inserted between bp 714 and 715 in the TIGR sequence.

- 15 6. Consequently, the TIGR DNA sequence incorrectly predicts that 3 amino acids are inserted into the GLC1A protein sequence.

- 20 6. A "T" is incorrectly inserted between bp #841 and #842 of the GLC1A DNA coding sequence in the TIGR sequence.

7. The "G" at bp #891 of the GLC1A DNA coding sequence is not present in the TIGR sequence.

25 Errors 6 and 7 cause 17 amino acids predicted by the GLC1A DNA coding sequence to be out of frame in the TIGR sequence.

- 30 8. A "G" at bp #979 of the GLC1A DNA coding sequence is replaced with a "C" in the TIGR sequence.

9. A "C" at bp #980 of the GLC1A DNA coding sequence is replaced with a "G" in the TIGR sequence.

Errors 8. and 9. cause the TIGR sequence to wrongly predict an arginine amino acid at residue #327 instead of an alanine.

5

The above 9 errors in the TIGR GLC1A sequence result in 45 nucleotide differences that cause 42 incorrect amino acid predictions. Therefore the human TIGR amino acid sequence is only about 91.67% identical to the human myocilin protein sequence and the human TIGR gene sequence is only about 97% identical to the human GLC1A sequence.

10

The identification of this disease gene increases the understanding of the pathophysiology of glaucoma, which in turn facilitates the development of assays for identifying molecules that modulate (e.g. agonize or antagonize) the bioactivity of a functional or mutant TIGR gene or protein. A therapeutically effective amount of these molecules can be administered to a subject with glaucoma or at risk for developing glaucoma to prevent or reduce the severity of the condition.

15

In addition, the establishment of the disease-causing nature of each GLC1A sequence variant and the associated penetrance and age of onset, as set forth herein, enables a clinician to provide patients, who harbor a particular sequence change, with useful information regarding their risk of developing glaucoma.

20

4.2 Definitions

For convenience, the meaning of certain terms and phrases employed in the specification, examples, and appended claims are provided below.

25

The term "agonist", as used herein, is meant to refer to an agent (e.g., a myocilin therapeutic) that directly or indirectly enhances, supplements or potentiates a wildtype or mutant myocilin bioactivity.

The term "antagonist", as used herein, is meant to refer to an agent (e.g. a myocilin therapeutic) that directly or indirectly prevents, minimizes or suppresses a wildtype or mutant myocilin bioactivity.

30

"Cells", "host cells" or "recombinant host cells" are terms used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or

environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A "chimeric protein" or "fusion protein" is a fusion of a first amino acid sequence encoding one of the subject polypeptides with a second amino acid sequence defining a domain (e.g. polypeptide portion) foreign to and not substantially homologous with any domain of one of the proteins. A chimeric protein may present a foreign domain which is found (albeit in a different protein) in an organism which also expresses the first protein, or it may be an "interspecies", "intergenic", etc. fusion of protein structures expressed by different kinds of organisms. In general, a fusion protein can be represented by the general formula X-myocilin-Y, wherein myocilin represents at least a portion of the protein which is derived from one of the myocilin proteins, and X and Y are independently absent or represent amino acid sequences which are not related to one of the myocilin sequences in an organism, including naturally occurring mutants.

"Complementary" sequences as used herein refer to sequences which have sufficient complementarity to be able to hybridize, forming a stable duplex.

A "delivery complex" shall mean a targeting means (e.g. a molecule that results in higher affinity binding of a gene, protein, polypeptide or peptide to a target cell surface and/or increased cellular uptake by a target cell). Examples of targeting means include: sterols (e.g. cholesterol), lipids (e.g. a cationic lipid, virosome or liposome), viruses (e.g. adenovirus, adeno-associated virus, and retrovirus) or target cell specific binding agents (e.g. ligands recognized by target cell specific receptors). Preferred complexes are sufficiently stable *in vivo* to prevent significant uncoupling prior to internalization by the target cell. However, the complex is cleavable under appropriate conditions within the cell so that the gene, protein, polypeptide or peptide is released in a functional form.

As is well known, genes for a particular polypeptide may exist in single or multiple copies within the genome of an individual. Such duplicate genes may be identical or may have certain modifications, including nucleotide substitutions, additions or deletions, which all still code for polypeptides having substantially the same activity. The term "DNA sequence encoding a myocilin polypeptide" may thus refer to one or more genes within a particular individual. Moreover, certain differences in nucleotide sequences may exist between individual organisms, which are called alleles. Such allelic differences may or may not result in differences in amino acid sequence of the encoded polypeptide yet still encode a protein with the same biological activity.

As used herein, the term "gene" or "recombinant gene" refers to a nucleic acid molecule comprising an open reading frame encoding one of the polypeptides of the present invention, including both exon and (optionally) intron sequences. A

"recombinant gene" refers to nucleic acid encoding a myocilin polypeptide and comprising GLC1A-encoding exon sequences, though it may optionally include intron sequences which are either derived from a chromosomal GLC1A gene or from an unrelated chromosomal gene. Exemplary recombinant genes encoding the subject myocilin polypeptides are represented in SEQ ID NO 7 and 9. The term "intron" refers to a DNA sequence present in a given GLC1A gene which is not translated into protein and is generally found between exons.

"Homology" or "identity" or "similarity" refers to sequence similarity between two peptides or between two nucleic acid molecules. Homology can be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same base or amino acid, then the molecules are homologous at that position. A degree of homology between sequences is a function of the number of matching or homologous positions shared by the sequences. An "unrelated" or "non-homologous" sequence shares less than 40 % identity, though preferably less than 25 % identity, with one of the GLC1A sequences of the present invention.

The term "interact" as used herein is meant to include detectable interactions between molecules, such as can be detected using, for example, a yeast two hybrid assay. The term interact is also meant to include "binding" interactions between molecules. Interactions may, for example, be protein-protein or protein-nucleic acid in nature.

The term "isolated" as used herein with respect to nucleic acids, such as DNA or RNA, refers to molecules separated from other DNAs, or RNAs, respectively, that are present in the natural source of the macromolecule. For example, an isolated nucleic acid encoding one of the subject GLC1A polypeptides preferably includes no more than 10 kilobases (kb) of nucleic acid sequence which naturally immediately flanks the GLC1A gene in genomic DNA, more preferably no more than 5kb of such naturally occurring flanking sequences, and most preferably less than 1.5kb of such naturally occurring flanking sequence. The term isolated as used herein also refers to a nucleic acid or peptide that is substantially free of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or

other chemicals when chemically synthesized. Moreover, an "isolated nucleic acid" is meant to include nucleic acid fragments which are not naturally occurring as fragments and would not be found in the natural state. The term "isolated" is also used herein to refer to polypeptides which are isolated from other cellular proteins and is meant to encompass both purified and recombinant polypeptides.

The term "modulation" as used herein refers to both upregulation, (i.e., activation or stimulation), for example by agonizing; and downregulation, (i.e. inhibition or suppression) for example by antagonizing a myocilin bioactivity.

A "myocilin bioactivity", "biological activity" or "activity" is meant to refer to a cytoskeletal or antigenic function that is directly or indirectly preformed by a myocilin polypeptide (whether in its native or denatured conformation), or by any subsequence thereof. Cytoskeletal functions include processes involved with the development or structure of ciliated neuroepithelium (e.g. comprising photoreceptor cells). Antigenic functions include possession of an epitope or antigenic site that is capable of cross-reacting with antibodies raised against a naturally occurring or denatured myocilin polypeptide or fragment thereof.

The "non-human animals" of the invention include mammals such as rodents, non-human primates, sheep, dog, cow, chickens, amphibians, reptiles, etc. Preferred non-human animals are selected from the rodent family including rat and mouse, most preferably mouse, though transgenic amphibians, such as members of the *Xenopus* genus, and transgenic chickens can also provide important tools for understanding and identifying agents which can affect, for example, embryogenesis and tissue formation. The term "chimeric animal" is used herein to refer to animals in which the recombinant gene is found, or in which the recombinant gene is expressed in some but not all cells of the animal. The term "tissue-specific chimeric animal" indicates that one of the recombinant GLC1A genes is present and/or expressed or disrupted in some tissues but not others.

As used herein, the term "nucleic acid" refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term should also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs, and, as applicable to the embodiment being described, single (sense or antisense) and double-stranded polynucleotides.

As used herein, the term "promoter" means a DNA sequence that regulates expression of a selected DNA sequence operably linked to the promoter, and

which effects expression of the selected DNA sequence in cells. The term encompasses "tissue specific" promoters, i.e. promoters, which effect expression of the selected DNA sequence only in specific cells (e.g. cells of a specific tissue). The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in one
5 tissue, but cause expression in other tissues as well. The term also encompasses non-tissue specific promoters and promoters that constitutively express or that are inducible (i.e. expression levels can be controlled).

The terms "protein", "polypeptide" and "peptide" are used interchangeably herein when referring to a gene product.

10 The term "recombinant protein" refers to a polypeptide of the present invention which is produced by recombinant DNA techniques, wherein generally, DNA encoding a myocilin polypeptide is inserted into a suitable expression vector which is in turn used to transform a host cell to produce the heterologous protein. Moreover, the phrase "derived from", with respect to a recombinant GLC1A gene, is meant to include
15 within the meaning of "recombinant protein" those proteins having an amino acid sequence of a native myocilin protein, or an amino acid sequence similar thereto which is generated by mutations including substitutions and deletions (including truncation) of a naturally occurring form of the protein.

"Small molecule" as used herein, is meant to refer to a composition,
20 which has a molecular weight of less than about 5kD and most preferably less than about 4kD. Small molecules can be nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic carbon containing or inorganic molecules. Extensive libraries of chemical or biological (e.g., fungal, bacterial or algal extracts) mixtures are available for screening with the assays of the invention.

25 As used herein, the term "specifically hybridizes" or "specifically detects" refers to the ability of a nucleic acid molecule of the invention to hybridize to at least approximately 6, 12, 20, 30, 50, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1460, 1470, 1480, 1490 consecutive nucleotides of a vertebrate, preferably
30 GLC1A gene, such as a GLC1A sequence designated in one of SEQ ID Nos: 7 or 9, or a sequence complementary thereto, or naturally occurring mutants thereof, such that it shows at least 10 times more hybridization, preferably at least 50 times more hybridization, and even more preferably at least 100 times more hybridization than it

does to a cellular nucleic acid (e.g., mRNA or genomic DNA) encoding a protein other than a vertebrate GLC1A protein as defined herein.

“Transcriptional regulatory sequence” is a generic term used throughout the specification to refer to DNA sequences, such as initiation signals, enhancers, and promoters, which induce or control transcription of protein coding sequences with which they are operably linked. In preferred embodiments, transcription of one of the recombinant GLC1A genes is under the control of a promoter sequence (or other transcriptional regulatory sequence) which controls the expression of the recombinant gene in a cell-type in which expression is intended. It will also be understood that the recombinant gene can be under the control of transcriptional regulatory sequences which are the same or which are different from those sequences which control transcription of the naturally-occurring forms of myocilin proteins.

As used herein, the term “transfection” means the introduction of a nucleic acid, e.g., an expression vector, into a recipient cell by nucleic acid-mediated gene transfer. “Transformation”, as used herein, refers to a process in which a cell's genotype is changed as a result of the cellular uptake of exogenous DNA or RNA, and, for example, the transformed cell expresses a recombinant form of a mammalian myocilin polypeptide or, in the case of anti-sense expression from the transferred gene, the expression of a naturally-occurring form of the myocilin protein is disrupted.

As used herein, the term “transgene” means a nucleic acid sequence (encoding, e.g., one of the mammalian myocilin polypeptides, or pending an antisense transcript thereto), which is partly or entirely heterologous, i.e., foreign, to the transgenic animal or cell into which it is introduced, or, is homologous to an endogenous gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or is inserted, into the animal's genome in such a way as to alter the genome of the cell into which it is inserted (e.g., it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). A transgene can include one or more transcriptional regulatory sequences and any other nucleic acid, such as introns, that may be necessary for optimal expression of a selected nucleic acid.

A “transgenic animal” refers to any animal, preferably a non-human mammal, bird or an amphibian, in which one or more of the cells of the animal contain heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate

genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or *in vitro* fertilization, but rather is directed to the introduction of a recombinant DNA molecule. This molecule may be integrated within a chromosome, or it may be
5 extrachromosomally replicating DNA. In the typical transgenic animals described herein, the transgene causes cells to express a recombinant form of one of the GLC1A proteins, e.g. either agonistic or antagonistic forms. However, transgenic animals in which the recombinant GLC1A gene is silent are also contemplated, as for example, the FLP or CRE recombinase dependent constructs described below. Moreover, "transgenic
10 animal" also includes those recombinant animals in which gene disruption of one or more GLC1A genes is caused by human intervention, including both recombination and antisense techniques.

The term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of preferred
15 vector is an episome, i.e., a nucleic acid capable of extra-chromosomal replication. Preferred vectors are those capable of autonomous replication and/or expression of nucleic acids to which they are linked. Vectors capable of directing the expression of genes to which they are operatively linked are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the
20 form of "plasmids" which refer generally to circular double stranded DNA loops which, in their vector form are not bound to the chromosome. In the present specification, "plasmid" and "vector" are used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors which serve equivalent functions and which become known in the art
25 subsequently hereto.

4.3 Nucleic Acids of the Present Invention

As described below, one aspect of the invention pertains to isolated nucleic acids comprising nucleotide sequences encoding myocilin polypeptides, and/or
30 equivalents of such nucleic acids. The term equivalent is understood to include nucleotide sequences encoding functionally equivalent myocilin polypeptides or functionally equivalent peptides having an activity of a vertebrate myocilin protein such as described herein. Equivalent nucleotide sequences will include sequences that differ by one or more nucleotide substitutions, additions or deletions, such as allelic variants;

and will, therefore, include sequences that differ from the nucleotide sequence of the GLC1A gene shown in SEQ ID Nos: 7 or 9 due to the degeneracy of the genetic code.

Preferred nucleic acids are vertebrate GLC1A nucleic acids. Particularly preferred vertebrate GLC1A nucleic acids are mammalian. Regardless of species, particularly preferred GLC1A nucleic acids encode polypeptides that are at least 90% similar to an amino acid sequence of human GLC1A. Preferred nucleic acids encode a GLC1A polypeptide comprising an amino acid sequence at least 90% homologous and more preferably 94% homologous with an amino acid sequence of a vertebrate GLC1A, e.g., such as a sequence shown in one of SEQ ID Nos: 8 or 10. Nucleic acids which encode polypeptides at least about 95%, and even more preferably at least about 98-99% similarity with an amino acid sequence represented in SEQ ID Nos.: 8 or 10 are also within the scope of the invention. In a particularly preferred embodiment, the nucleic acid of the present invention encodes an amino acid GLC1A sequence shown in one of SEQ ID No: 8 or 10. In one embodiment, the nucleic acid is a cDNA encoding a peptide having at least one bioactivity of the subject GLC1A polypeptide. Preferably, the nucleic acid includes all or a portion of the nucleotide sequence corresponding to the coding region of SEQ ID Nos: 1-7 or 9.

Still other preferred nucleic acids of the present invention encode a GLC1A polypeptide which includes a polypeptide sequence corresponding to all or a portion of amino acid residues of SEQ ID Nos: 8 or 10, e.g., at least 2, 5, 10, 25, 50, 100, 150 or 200 amino acid residues of that region. For example, preferred nucleic acid molecules for use as probes/primer or antisense molecules (i.e. noncoding nucleic acid molecules) can comprise at least about 6, 12, 20, 30, 50, 100, 125, 150 or 200 base pairs in length, whereas coding nucleic acid molecules can comprise about 200, 250, 300, 350, 400, 410, 420, 430, 435 or 440 base pairs.

Another aspect of the invention provides a nucleic acid which hybridizes to a nucleic acid represented by one of SEQ ID Nos: 1-7 or 9. Appropriate stringency conditions which promote DNA hybridization, for example, 6.0 x sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 x SSC at 50°C, are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 x SSC at 50°C to a high stringency of about 0.2 x SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature,

about 22°C, to high stringency conditions at about 65°C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed. In a preferred embodiment, a GLC1A nucleic acid of the present invention will bind to one of SEQ ID Nos 1 or 2 under moderately stringent
5 conditions, for example at about 2.0 x SSC and about 40°C. In a particularly preferred embodiment, a GLC1A nucleic acid of the present invention will bind to one of SEQ ID Nos: 1-7 or 9 under high stringency conditions.

Preferred nucleic acids have a sequence at least about 75% homologous and more preferably 80% and even more preferably at least about 85% homologous with
10 an amino acid sequence of a mammalian GLC1A, e.g., such as a sequence shown in one of SEQ ID Nos: 8 and 10. Nucleic acids at least about 90%, more preferably about 95%, and most preferably at least about 98-99% homologous with a nucleic sequence represented in one of SEQ ID Nos: 8 and 10 are of course also within the scope of the invention. In preferred embodiments, the nucleic acid is a mammalian GLC1A gene and
15 in particularly preferred embodiments, includes all or a portion of the nucleotide sequence corresponding to the coding region of one of SEQ ID Nos: 1-7 or 9.

Nucleic acids having a sequence that differs from the nucleotide sequences shown in one of SEQ ID Nos: 1-7 or 9 due to degeneracy in the genetic code are also within the scope of the invention. Such nucleic acids encode functionally
20 equivalent peptides (i.e., a peptide having a biological activity of a myocilin polypeptide) but differ in sequence from the sequence shown in the sequence listing due to degeneracy in the genetic code. For example, a number of amino acids are designated by more than one triplet. Codons that specify the same amino acid, or synonyms (for example, CAU and CAC each encode histidine) may result in "silent" mutations which
25 do not affect the amino acid sequence of a myocilin polypeptide. However, it is expected that DNA sequence polymorphisms that do lead to changes in the amino acid sequences of the subject myocilin polypeptides will exist among mammals. One skilled in the art will appreciate that these variations in one or more nucleotides (e.g., up to about 3-5% of the nucleotides) of the nucleic acids encoding polypeptides having an
30 activity of a mammalian myocilin polypeptide may exist among individuals of a given species due to natural allelic variation.

As indicated by the examples set out below, myocilin protein-encoding nucleic acids can be obtained from mRNA present in any of a number of eukaryotic cells. It should also be possible to obtain nucleic acids encoding mammalian myocilin

polypeptides of the present invention from genomic DNA from both adults and embryos. For example, a gene encoding a myocilin protein can be cloned from either a cDNA or a genomic library in accordance with protocols described herein, as well as those generally known to persons skilled in the art. Examples of tissues and/or libraries suitable for isolation of the subject nucleic acids include photoreceptor cells of the retina, among others. A cDNA encoding a myocilin protein can be obtained by isolating total mRNA from a cell, e.g. a vertebrate cell, a mammalian cell, or a human cell, including embryonic cells. Double stranded cDNAs can then be prepared from the total mRNA, and subsequently inserted into a suitable plasmid or bacteriophage vector using any one of a number of known techniques. The gene encoding a mammalian myocilin protein can also be cloned using established polymerase chain reaction techniques in accordance with the nucleotide sequence information provided by the invention. The nucleic acid of the invention can be DNA or RNA. A preferred nucleic acid is a cDNA represented by a sequence selected from the group consisting of SEQ ID Nos:1 and 2.

4.3.1. Vectors.

This invention also provides expression vectors containing a nucleic acid encoding a myocilin polypeptide, operably linked to at least one transcriptional regulatory sequence. "Operably linked" is intended to mean that the nucleotide sequence is linked to a regulatory sequence in a manner which allows expression of the nucleotide sequence. Regulatory sequences are art-recognized and are selected to direct expression of the subject mammalian myocilin proteins. Accordingly, the term "transcriptional regulatory sequence" includes promoters, enhancers and other expression control elements. Such regulatory sequences are described in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). In one embodiment, the expression vector includes a recombinant gene encoding a peptide having an agonistic activity of a subject myocilin polypeptide, or alternatively, encoding a peptide which is an antagonistic form of the myocilin protein. Such expression vectors can be used to transfect cells and thereby produce polypeptides, including fusion proteins, encoded by nucleic acids as described herein. Moreover, the gene constructs of the present invention can also be used as a part of a gene therapy protocol to deliver nucleic acids encoding either an agonistic or antagonistic form of one of the subject myocilin proteins. Thus, another aspect of the invention features expression vectors for *in vivo* or *in vitro* transfection and expression of a myocilin

polypeptide in particular cell types so as to reconstitute the function of, or alternatively, abrogate the function of myocilin-induced signaling in a tissue. This could be desirable, for example, when the naturally-occurring form of the protein is misexpressed; or to deliver a form of the protein which alters differentiation of tissue. Expression vectors
5 may also be employed to inhibit neoplastic transformation.

In addition to viral transfer methods, such as those illustrated above, non-viral methods can also be employed to cause expression of a subject myocilin polypeptide in the tissue of an animal. Most nonviral methods of gene transfer rely on normal mechanisms used by mammalian cells for the uptake and intracellular transport
10 of macromolecules. In preferred embodiments, non-viral targeting means of the present invention rely on endocytic pathways for the uptake of the subject myocilin polypeptide gene by the targeted cell. Exemplary targeting means of this type include liposomal derived systems, poly-lysine conjugates, and artificial viral envelopes.

15 4.3.2. Probes and Primers

Moreover, the nucleotide sequences determined from the cloning of GLC1A genes from mammalian organisms will further allow for the generation of probes and primers designed for use in identifying and/or cloning homologs in other cell types, e.g. from other tissues, as well as homologs from other mammalian organisms.
20 For instance, the present invention also provides a probe/primer comprising a substantially purified oligonucleotide, which oligonucleotide comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least approximately 12, preferably 25, more preferably 40, 50 or 75 consecutive nucleotides of sense or anti-sense sequence selected from the group consisting of SEQ ID Nos: 1-7 or 9, or naturally
25 occurring mutants thereof. For instance, primers based on the nucleic acid represented in SEQ ID Nos: 1-7 or 9 can be used in PCR reactions to clone homologs. Preferred primer pairs of the invention are set forth as SEQ ID Nos. 12 and 13; 14 and 15; 16 and 17; 18 and 19; 20 and 21; 22 and 23; 24 and 25; 26 and 27; 28 and 29; 30 and 31; 32 and 33; 34 and 35; 36 and 37; 38 and 39; 40 and 41; 42 and 43; 44 and 45; and 46 and 47.

30 Likewise, probes based on the subject GLC1A sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto and able to be detected, e.g. the label group can be selected from amongst radioisotopes, fluorescent compounds, enzymes, and enzyme co-factors, etc.

As discussed in more detail below, such probes can also be used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a myocilin protein, such as by measuring a level of a myocilin -encoding nucleic acid in a sample of cells from a patient; e.g. detecting GLC1A mRNA levels or determining whether a genomic GLC1A gene has been mutated or deleted. Briefly, nucleotide probes can be generated from the subject GLC1A genes which facilitate histological screening of intact tissue and tissue samples for the presence (or absence) of myocilin-encoding transcripts. Similar to the diagnostic uses of anti-myocilin antibodies, the use of probes directed to GLC1A messages, or to genomic GLC1A sequences, can be used for both predictive and therapeutic evaluation of subjects. Used in conjunction with immunoassays as described herein, the oligonucleotide probes can help facilitate the determination of the molecular basis for a developmental disorder which may involve some abnormality associated with expression (or lack thereof) of a myocilin protein. For instance, variation in polypeptide synthesis can be differentiated from a mutation in a coding sequence.

4.3.3. Antisense, Ribozyme and Triplex Techniques

One aspect of the invention relates to the use of the isolated nucleic acid in "antisense" therapy. As used herein, "antisense" therapy refers to administration or *in situ* generation of oligonucleotide molecules or their derivatives which specifically hybridize (e.g. bind) under cellular conditions, with the cellular mRNA and/or genomic DNA encoding one or more of the subject GLC1A proteins so as to inhibit expression of that protein, e.g. by inhibiting transcription and/or translation. The binding may be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interactions in the major groove of the double helix. In general, "antisense" therapy refers to the range of techniques generally employed in the art, and includes any therapy which relies on specific binding to oligonucleotide sequences.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid which, when transcribed in the cell, produces RNA which is complementary to at least a unique portion of the cellular mRNA which encodes a myocilin protein. Alternatively, the antisense construct is an oligonucleotide probe which is generated *ex vivo* and which, when introduced into the cell causes inhibition of expression by hybridizing with the mRNA and/or genomic sequences of a GLC1A gene. Such oligonucleotide probes are preferably modified oligonucleotides

which are resistant to endogenous nucleases, e.g. exonucleases and/or endonucleases, and are therefore stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Patents 5,176,996; 5,264,564; and 5,256,775). Additionally,
5 general approaches to constructing oligomers useful in antisense therapy have been reviewed, for example, by Van der Krol et al. (1988) *Biotechniques* 6:958-976; and Stein et al. (1988) *Cancer Res* 48:2659-2668. With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site, e.g., between the -10 and +10 regions of the GLC1A nucleotide sequence of interest, are preferred.

10 Antisense approaches involve the design of oligonucleotides (either DNA or RNA) that are complementary to GLC1A mRNA. The antisense oligonucleotides will bind to the GLC1A mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, means a sequence having sufficient
15 complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an
20 RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Oligonucleotides that are complementary to the 5' end of the message, e.g., the 5' untranslated sequence up to and including the AUG initiation codon, should
25 work most efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated sequences of mRNAs have recently been shown to be effective at inhibiting translation of mRNAs as well. (Wagner, R. 1994. *Nature* 372:333). Therefore, oligonucleotides complementary to either the 5' or 3' untranslated, non-coding regions of a GLC1A gene could be used in an antisense approach to inhibit
30 translation of endogenous GLC1A mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are less efficient inhibitors of translation but could be used in accordance with the invention. Whether designed to hybridize to the 5', 3' or coding region of GLC1A mRNA, antisense

nucleic acids should be at least six nucleotides in length, and are preferably oligonucleotides ranging from 6 to about 50 nucleotides in length. In certain embodiments, the oligonucleotide is at least 10 nucleotides, at least 17 nucleotides, at least 25 nucleotides, or at least 50 nucleotides.

5 Regardless of the choice of target sequence, it is preferred that *in vitro* studies are first performed to quantitate the ability of the antisense oligonucleotide to quantitate the ability of the antisense oligonucleotide to inhibit gene expression. It is preferred that these studies utilize controls that distinguish between antisense gene inhibition and nonspecific biological effects of oligonucleotides. It is also preferred that
10 these studies compare levels of the target RNA or protein with that of an internal control RNA or protein. Additionally, it is envisioned that results obtained using the antisense oligonucleotide are compared with those obtained using a control oligonucleotide. It is preferred that the control oligonucleotide is of approximately the same length as the test oligonucleotide and that the nucleotide sequence of the oligonucleotide differs from the
15 antisense sequence no more than is necessary to prevent specific hybridization to the target sequence.

 The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate
20 backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger et al., 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre et al., 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. WO 88/09810,
25 published December 15, 1988) or the blood-brain barrier (see, *e.g.*, PCT Publication No. WO 89/10134, published April 25, 1988), hybridization-triggered cleavage agents. (See, *e.g.*, Krol et al., 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, hybridization triggered cross-linking agent, transport
30 agent, hybridization-triggered cleavage agent, etc.

 The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine,

5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, 5 beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including but not limited to arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet another embodiment, the antisense oligonucleotide is an α -anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual conformation, the strands run parallel to each other (Gautier et al., 1987, *Nucl. Acids Res.* 15:6625-6641). The oligonucleotide is a 2'-O-methylribonucleotide (Inoue et al., 1987, *Nucl. Acids Res.* 15:6131-6148), or a chimeric RNA-DNA analogue (Inoue et al., 1987, *FEBS Lett.* 215:327-330).

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g. by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (1988, *Nucl. Acids Res.* 16:3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85:7448-7451), etc.

While antisense nucleotides complementary to the GLC1A coding region sequence could be used, those complementary to the transcribed untranslated region are most preferred.

5 The antisense molecules should be delivered to cells which express the myocilin *in vivo*. A number of methods have been developed for delivering antisense DNA or RNA to cells; *e.g.*, antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systematically.

10 However, it is often difficult to achieve intracellular concentrations of the antisense sufficient to suppress translation of endogenous mRNAs. Therefore a preferred approach utilizes a recombinant DNA construct in which the antisense oligonucleotide is placed under the control of a strong pol III or pol II promoter. The use of such a construct to transfect target cells in the patient will result in the
15 transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous GLC1A transcripts and thereby prevent translation of the GLC1A mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be
20 transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequence encoding the antisense RNA can be by any promoter known in the art to act in mammalian, preferably human cells. Such promoters can be inducible
25 or constitutive. Such promoters include but are not limited to: the SV40 early promoter region (Bernoist and Chambon, 1981, *Nature* 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., 1980, *Cell* 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, *Proc. Natl. Acad. Sci. U.S.A.* 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, *Nature* 296:39-42), etc. Any type of plasmid, cosmid, YAC or viral vector can
30 be used to prepare the recombinant DNA construct which can be introduced directly into the tissue site; *e.g.*, the choroid plexus or hypothalamus. Alternatively, viral vectors can be used which selectively infect the desired tissue; (*e.g.*, for brain, herpesvirus vectors

may be used), in which case administration may be accomplished by another route (e.g., systematically).

Ribozyme molecules designed to catalytically cleave GLC1A mRNA transcripts can also be used to prevent translation of GLC1A mRNA and expression of myocilin. (See, e.g., PCT International Publication WO 90/11364, published October 4, 1990; Sarver et al., 1990, *Science* 247:1222-1225). While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy GLC1A mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, 1988, *Nature*, 334:585-591. There are hundreds of potential hammerhead ribozyme cleavage sites within the nucleotide sequence of human GLC1A cDNA. Preferably the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the GLC1A mRNA; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

The ribozymes of the present invention also include RNA endoribonucleases (hereinafter "Cech-type ribozymes") such as the one which occurs naturally in *Tetrahymena Thermophila* (known as the IVS, or L-19 IVS RNA) and which has been extensively described by Thomas Cech and collaborators (Zaug, et al., 1984, *Science*, 224:574-578; Zaug and Cech, 1986, *Science*, 231:470-475; Zaug, et al., 1986, *Nature*, 324:429-433; published International patent application No. WO 88/04300 by University Patents Inc.; Been and Cech, 1986, *Cell*, 47:207-216). The Cech-type ribozymes have an eight base pair active site which hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. The invention encompasses those Cech-type ribozymes which target eight base-pair active site sequences that are present in GLC1A.

As in the antisense approach, the ribozymes can be composed of modified oligonucleotides (e.g. for improved stability, targeting, etc.) and should be delivered to cells which express the GLC1A *in vivo* e.g., hypothalamus and/or the choroid plexus. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to

destroy endogenous GLC1A messages and inhibit translation. Because ribozymes unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Endogenous GLC1A gene expression can also be reduced by inactivating or "knocking out" the GLC1A gene or its promoter using targeted homologous recombination. (e.g, see Smithies et al., 1985, *Nature* 317:230-234; Thomas & Capecchi, 1987, *Cell* 51:503-512; Thompson et al., 1989 *Cell* 5:313-321; each of which is incorporated by reference herein in its entirety). For example, a mutant, non-functional GLC1A (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous GLC1A gene (either the coding regions or regulatory regions of the GLC1A gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express GLC1A *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the GLC1A gene. Such approaches are particularly suited in the agricultural field where modifications to ES (embryonic stem) cells can be used to generate animal offspring with an inactive GLC1A (e.g., see Thomas & Capecchi 1987 and Thompson 1989, *supra*). However this approach can be adapted for use in humans provided the recombinant DNA constructs are directly administered or targeted to the required site *in vivo* using appropriate viral vectors, e.g., herpes virus vectors for delivery to brain tissue; e.g., the hypothalamus and/or choroid plexus.

Alternatively, endogenous GLC1A gene expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of the GLC1A gene (i.e., the GLC1A promoter and/or enhancers) to form triple helical structures that prevent transcription of the GLC1A gene in target cells in the body. (See generally, Helene, C. 1991, *Anticancer Drug Des.*, 6(6):569-84; Helene, C., et al., 1992, *Ann. N.Y. Acad. Sci.*, 660:27-36; and Maher, L.J., 1992, *Bioassays* 14(12):807-15).

Likewise, the antisense constructs of the present invention, by antagonizing the normal biological activity of one of the myocilin proteins, can be used in the manipulation of tissue, e.g. tissue differentiation, both *in vivo* and for *ex vivo* tissue cultures.

Furthermore, the anti-sense techniques (e.g. microinjection of antisense molecules, or transfection with plasmids whose transcripts are antisense with regard to a GLC1A mRNA or gene sequence) can be used to investigate role of myocilin in developmental events, as well as the normal cellular function of myocilin in adult tissue.

Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals, as detailed below.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA, followed by an endonucleolytic cleavage. The composition of ribozyme molecules must include one or more sequences complementary to the target gene mRNA, and must include the well known catalytic sequence responsible for mRNA cleavage. For this sequence, see U.S. Pat. No. 5,093,246, which is incorporated by reference herein in its entirety. As such within the scope of the invention are engineered hammerhead motif ribozyme molecules that specifically and efficiently catalyze endonucleolytic cleavage of RNA sequences encoding myocilin proteins.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the molecule of interest for ribozyme cleavage sites which include the following sequences, GUA, GUU and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides corresponding to the region of the target gene containing the cleavage site may be evaluated for predicted structural features, such as secondary structure, that may render the oligonucleotide sequence unsuitable. The suitability of candidate sequences may also be evaluated by testing their accessibility to hybridization with complementary oligonucleotides, using ribonuclease protection assays.

Nucleic acid molecules to be used in triple helix formation for the inhibition of transcription are preferably single stranded and composed of deoxyribonucleotides. The base composition of these oligonucleotides should promote triple helix formation via Hoogsteen base pairing rules, which generally require sizable stretches of either purines or pyrimidines to be present on one strand of a duplex. Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine-rich, for example, containing a stretch of G residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in CGC triplets across the three strands in the triplex.

Alternatively, the potential sequences that can be targeted for triple helix formation may be increased by creating a so called "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizable stretch of either purines or pyrimidines to be present on one strand of a duplex.

Antisense RNA and DNA, ribozyme, and triple helix molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

Moreover, various well-known modifications to nucleic acid molecules may be introduced as a means of increasing intracellular stability and half-life. Possible modifications include but are not limited to the addition of flanking sequences of ribonucleotides or deoxyribonucleotides to the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the oligodeoxyribonucleotide backbone.

4.4. Polypeptides of the Present Invention

The present invention also makes available myocilin polypeptides, which are isolated from, or otherwise substantially free of other cellular proteins, especially other signal transduction factors and/or transcription factors which may normally be associated with the myocilin polypeptide. The term "substantially free of other cellular proteins" (also referred to herein as "contaminating proteins") or "substantially pure or purified preparations" are defined as encompassing preparations of myocilin polypeptides having less than about 20% (by dry weight) contaminating protein, and preferably having less than about 5% contaminating protein. Functional forms of the subject polypeptides can be prepared, for the first time, as purified preparations by using a cloned gene as described herein. By "purified", it is meant, when referring to a peptide or DNA or RNA sequence,

that the indicated molecule is present in the substantial absence of other biological macromolecules, such as other proteins. The term "purified" as used herein preferably means at least 80% by dry weight, more preferably in the range of 95-99% by weight, and most preferably at least 99.8% by weight, of biological macromolecules of the same type present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 5000, can be present). The term "pure" as used herein preferably has the same numerical limits as "purified" immediately above. "Isolated" and "purified" do not encompass either natural materials in their native state or natural materials that have been separated into components (e.g., in an acrylamide gel) but not obtained either as pure (e.g. lacking contaminating proteins, or chromatography reagents such as denaturing agents and polymers, e.g. acrylamide or agarose) substances or solutions. In preferred embodiments, purified GLC1A preparations will lack any contaminating proteins from the same animal from which myocilin is normally produced, as can be accomplished by recombinant expression of, for example, a human myocilin protein in a non-human cell.

Full length proteins or fragments corresponding to one or more particular motifs and/or domains or to arbitrary sizes, for example, at least 5, 10, 25, 50, 75, 100, 125, 150 amino acids in length are within the scope of the present invention.

For example, isolated myocilin polypeptides can include all or a portion of an amino acid sequences corresponding to a myocilin polypeptide represented in SEQ ID Nos: 8 or 10. Isolated peptidyl portions of myocilin proteins can be obtained by screening peptides recombinantly produced from the corresponding fragment of the nucleic acid encoding such peptides. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, a myocilin polypeptide of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or preferably divided into overlapping fragments of a desired length. The fragments can be produced (recombinantly or by chemical synthesis) and tested to identify those peptidyl fragments which can function as either agonists or antagonists of a wild-type (e.g., "authentic") myocilin protein.

Another aspect of the present invention concerns recombinant forms of the myocilin proteins. Recombinant polypeptides preferred by the present invention, in addition to native myocilin proteins, are at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% homologous with an amino acid sequence represented by SEQ ID Nos: 8 or 10. In a preferred embodiment, a myocilin protein of the present invention is a myocilin

protein. In a particularly preferred embodiment, a myocilin protein comprises the coding sequence of one of SEQ ID No.: 1-7, or 9. In particularly preferred embodiments, a myocilin protein has a myocilin bioactivity.

5 The present invention further pertains to recombinant forms of one of the subject myocilin polypeptides which are encoded by genes derived from a mammalian organism, and which have amino acid sequences evolutionarily related to the myocilin proteins represented in SEQ ID Nos: 8 or 10. Such recombinant myocilin polypeptides preferably are capable of functioning in one of either role of an agonist or antagonist of at least one biological activity of a wild-type ("authentic") myocilin protein of the appended
10 sequence listing. The term "evolutionarily related to", with respect to amino acid sequences of myocilin proteins, refers to both polypeptides having amino acid sequences which have arisen naturally, and also to mutational variants of myocilin polypeptides which are derived, for example, by combinatorial mutagenesis. Such evolutionarily derived myocilin polypeptides preferred by the present invention have a myocilin bioactivity and are at least
15 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous with the amino acid sequence selected from the group consisting of SEQ ID Nos: 8 or 10.

In general, polypeptides referred to herein as having an activity of a myocilin protein (e.g., are "bioactive") are defined as polypeptides which include an amino acid sequence corresponding (e.g., identical or homologous) to all or a portion of the amino acid
20 sequences of a myocilin protein shown in SEQ ID Nos: 8 or 10 and which mimic or antagonize all or a portion of the biological/biochemical activities of a naturally occurring myocilin protein. According to the present invention, a polypeptide has biological activity if it is a specific agonist or antagonist of a naturally-occurring form of a myocilin protein.

The present invention further pertains to methods of producing the subject
25 myocilin polypeptides. For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding the subject polypeptides can be cultured under appropriate conditions to allow expression of the peptide to occur. The cells may be harvested, lysed and the protein isolated. A cell culture includes host cells, media and other byproducts. Suitable media for cell culture are well known in the art. The
30 recombinant myocilin polypeptide can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such peptide. In a preferred

embodiment, the recombinant myocilin polypeptide is a fusion protein containing a domain which facilitates its purification, such as GST fusion protein or poly(His) fusion protein.

Moreover, it will be generally appreciated that, under certain circumstances, it may be advantageous to provide homologs of one of the subject myocilin polypeptides which function in a limited capacity as one of either a myocilin agonist (mimetic) or a myocilin antagonist, in order to promote or inhibit only a subset of the biological activities of the naturally-occurring form of the protein. Thus, specific biological effects can be elicited by treatment with a homolog of limited function, and with fewer side effects relative to treatment with agonists or antagonists which are directed to all of the biological activities of naturally occurring forms of myocilin proteins.

Homologs of each of the subject myocilin proteins can be generated by mutagenesis, such as by discrete point mutation(s), or by truncation. For instance, mutation can give rise to homologs which retain substantially the same, or merely a subset, of the biological activity of the myocilin polypeptide from which it was derived. Alternatively, antagonistic forms of the protein can be generated which are able to inhibit the function of the naturally occurring form of the protein, such as by competitively binding to a downstream or upstream member of the biochemical pathway, which includes the myocilin protein. In addition, agonistic forms of the protein may be generated which are constitutively active. Thus, the human myocilin protein and homologs thereof provided by the subject invention may be either positive or negative regulators of gene expression.

The recombinant myocilin polypeptides of the present invention also include homologs of the authentic myocilin proteins, such as versions of those protein which are resistant to proteolytic cleavage, as for example, due to mutations which alter ubiquitination or other enzymatic targeting associated with the protein.

Myocilin polypeptides may also be chemically modified to create derivatives by forming covalent or aggregate conjugates with other chemical moieties, such as glycosyl groups, lipids, phosphate, acetyl groups and the like. Covalent derivatives of myocilin proteins can be prepared by linking the chemical moieties to functional groups on amino acid sidechains of the protein or at the N-terminus or at the C-terminus of the polypeptide.

Modification of the structure of the subject myocilin polypeptides can be for such purposes as enhancing therapeutic or prophylactic efficacy, stability (e.g., *ex vivo* shelf life and resistance to proteolytic degradation *in vivo*), or post-translational modifications (e.g., to alter phosphorylation pattern of protein). Such modified peptides, when designed to retain at least one activity of the naturally-occurring form of the protein, or to produce

specific antagonists thereof, are considered functional equivalents of the myocilin polypeptides described in more detail herein. Such modified peptides can be produced, for instance, by amino acid substitution, deletion, or addition.

For example, it is reasonable to expect that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid (i.e. isosteric and/or isoelectric mutations) will not have a major effect on the biological activity of the resulting molecule. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids are can be divided into four families: (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine, histidine; (3) nonpolar = alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar = glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. In similar fashion, the amino acid repertoire can be grouped as (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine histidine, (3) aliphatic = glycine, alanine, valine, leucine, isoleucine, serine, threonine, with serine and threonine optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic = phenylalanine, tyrosine, tryptophan; (5) amide = asparagine, glutamine; and (6) sulfur - containing = cysteine and methionine. (see, for example, *Biochemistry*, 2nd ed., Ed. by L. Stryer, WH Freeman and Co.: 1981). Whether a change in the amino acid sequence of a peptide results in a functional myocilin homolog (e.g. functional in the sense that the resulting polypeptide mimics or antagonizes the wild-type form) can be readily determined by assessing the ability of the variant peptide to produce a response in cells in a fashion similar to the wild-type protein, or competitively inhibit such a response. Polypeptides in which more than one replacement has taken place can readily be tested in the same manner.

This invention further contemplates a method for generating sets of combinatorial mutants of the subject myocilin proteins as well as truncation mutants, and is especially useful for identifying potential variant sequences (e.g. homologs) that are functional in modulating gene expression. The purpose of screening such combinatorial libraries is to generate, for example, novel myocilin homologs which can act as either agonists or antagonist, or alternatively, possess novel activities all together.

Likewise, myocilin homologs can be generated by the present combinatorial approach to selectively inhibit gene expression. For instance, mutagenesis can provide myocilin homologs which are able to bind other signal pathway proteins (or DNA) yet prevent propagation of the signal, e.g. the homologs can be dominant negative mutants.

Moreover, manipulation of certain domains of myocilin by the present method can provide domains more suitable for use in fusion proteins.

In one embodiment, the variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For instance, a mixture of synthetic oligonucleotides can be enzymatically ligated
5 into gene sequences such that the degenerate set of potential GLC1A sequences are expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g. for phage display) containing the set of GLC1A sequences therein.

There are many ways by which such libraries of potential myocilin homologs
10 can be generated from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an appropriate expression vector. The purpose of a degenerate set of genes is to provide, in one mixture, all of the sequences encoding the desired set of potential myocilin sequences. The synthesis of degenerate oligonucleotides
15 is well known in the art (see for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton, Amsterdam: Elsevier ppg. 273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for
20 example, Scott et al. (1990) *Science* 249:386-390; Roberts et al. (1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

Likewise, a library of coding sequence fragments can be provided for a GLC1A clone in order to generate a variegated population of myocilin fragments for
25 screening and subsequent selection of bioactive fragments. A variety of techniques are known in the art for generating such libraries, including chemical synthesis. In one embodiment, a library of coding sequence fragments can be generated by (i) treating a double stranded PCR fragment of a GLC1A coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule; (ii) denaturing the double
30 stranded DNA; (iii) renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products; (iv) removing single stranded portions from reformed duplexes by treatment with S1 nuclease; and (v) ligating the resulting fragment library into an expression vector. By this exemplary method, an expression library

can be derived which codes for N-terminal, C-terminal and internal fragments of various sizes.

A wide range of techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a certain property. Such techniques will be generally adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of GLC1A homologs. The most widely used techniques for screening large gene libraries typically comprises cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the illustrative assays described below are amenable to high through-put analysis as necessary to screen large numbers of degenerate GLC1A sequences created by combinatorial mutagenesis techniques. Combinatorial mutagenesis has a potential to generate very large libraries of mutant proteins, e.g., in the order of 10^{26} molecules. Combinatorial libraries of this size may be technically challenging to screen even with high throughput screening assays. To overcome this problem, a new technique has been developed recently, recursive ensemble mutagenesis (REM), which allows one to avoid the very high proportion of non-functional proteins in a random library and simply enhances the frequency of functional proteins, thus decreasing the complexity required to achieve a useful sampling of sequence space. REM is an algorithm which enhances the frequency of functional mutants in a library when an appropriate selection or screening method is employed (Arkin and Yourvan, 1992, *PNAS USA* 89:7811-7815; Yourvan et al., 1992, *Parallel Problem Solving from Nature*, 2., In Maenner and Manderick, eds., Elsevier Publishing Co., Amsterdam, pp. 401-410; Delgrave et al., 1993, *Protein Engineering* 6(3):327-331).

The invention also provides for reduction of the myocilin proteins to generate mimetics, e.g. peptide or non-peptide agents, which are able to disrupt binding of a mammalian myocilin polypeptide of the present invention with either upstream or downstream components. Thus, such mutagenic techniques as described above are also useful to map the determinants of the myocilin proteins which participate in protein-protein interactions involved in, for example, binding of the subject myocilin polypeptide to proteins which may function upstream (including both activators and repressors of its activity) or to proteins or nucleic acids which may function downstream of the myocilin

polypeptide, whether they are positively or negatively regulated by it. To illustrate, the critical residues of a subject myocilin polypeptide which are involved in molecular recognition of a component upstream or downstream of myocilin can be determined and used to generate myocilin-derived peptidomimetics which competitively inhibit binding of the authentic myocilin protein with that moiety. By employing, for example, scanning mutagenesis to map the amino acid residues of each of the subject myocilin proteins which are involved in binding other extracellular proteins, peptidomimetic compounds can be generated which mimic those residues of the myocilin protein which facilitate the interaction. Such mimetics may then be used to interfere with the normal function of a myocilin protein. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gamma lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), β -turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans* 1:1231), and b-aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun* 126:419; and Dann et al. (1986) *Biochem Biophys Res Commun* 134:71).

4.4.1. Cells expressing recombinant myocilin polypeptides.

This invention also pertains to a host cell transfected to express a recombinant form of the subject myocilin polypeptides. The host cell may be any prokaryotic or eukaryotic cell. Thus, a nucleotide sequence derived from the cloning of myocilin proteins, encoding all or a selected portion of the full-length protein, can be used to produce a recombinant form of a myocilin polypeptide via microbial or eukaryotic cellular processes. Ligating the polynucleotide sequence into a gene construct, such as an expression vector, and transforming or transfecting into hosts, either eukaryotic (yeast, avian, insect or mammalian) or prokaryotic (bacterial) cells, are standard procedures used in producing other well-known proteins, e.g. MAP kinase, pg. 53, WT1, PTP phosphatases, SRC, and the like. Similar procedures, or modifications thereof, can be employed to

prepare recombinant myocilin polypeptides by microbial means or tissue-culture technology in accord with the subject invention.

The recombinant GLC1A genes can be produced by ligating nucleic acid encoding a myocilin protein, or a portion thereof, into a vector suitable for expression in either prokaryotic cells, eukaryotic cells, or both. Expression vectors for production of recombinant forms of the subject myocilin polypeptides include plasmids and other vectors. For instance, suitable vectors for the expression of a myocilin polypeptide include plasmids of the types: pBR322-derived plasmids, pEMBL-derived plasmids, pEX-derived plasmids, pBTac-derived plasmids and pUC-derived plasmids for expression in prokaryotic cells, such as *E. coli*.

A number of vectors exist for the expression of recombinant proteins in yeast. For instance, YEP24, YIP5, YEP51, YEP52, pYES2, and YRP17 are cloning and expression vehicles useful in the introduction of genetic constructs into *S. cerevisiae* (see, for example, Broach *et al.* (1983) in *Experimental Manipulation of Gene Expression*, ed. M. Inouye Academic Press, p. 83, incorporated by reference herein). These vectors can replicate in *E. coli* due the presence of the pBR322 ori, and in *S. cerevisiae* due to the replication determinant of the yeast 2 micron plasmid. In addition, drug resistance markers such as ampicillin can be used. In an illustrative embodiment, a myocilin polypeptide is produced recombinantly utilizing an expression vector generated by sub-cloning the coding sequence of one of the GLC1A genes represented in SEQ ID Nos: 1-7 or 9.

The preferred mammalian expression vectors contain both prokaryotic sequences, to facilitate the propagation of the vector in bacteria, and one or more eukaryotic transcription units that are expressed in eukaryotic cells. The pcDNAI/amp, pcDNAI/neo, pRc/CMV, pSV2gpt, pSV2neo, pSV2-dhfr, pTk2, pRSVneo, pMSG, pSVT7, pko-neo and pHyg derived vectors are examples of mammalian expression vectors suitable for transfection of eukaryotic cells. Some of these vectors are modified with sequences from bacterial plasmids, such as pBR322, to facilitate replication and drug resistance selection in both prokaryotic and eukaryotic cells. Alternatively, derivatives of viruses such as the bovine papillomavirus (BPV-1), or Epstein-Barr virus (pHEBo, pREP-derived and p205) can be used for transient expression of proteins in eukaryotic cells. The various methods employed in the preparation of the plasmids and transformation of host organisms are well known in the art. For other suitable expression systems for both prokaryotic and eukaryotic cells, as well as general recombinant procedures, see *Molecular Cloning A*

Laboratory Manual, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989) Chapters 16 and 17.

5 In some instances, it may be desirable to express the recombinant myocilin polypeptide by the use of a baculovirus expression system. Examples of such baculovirus expression systems include pVL-derived vectors (such as pVL1392, pVL1393 and pVL941), pAcUW-derived vectors (such as pAcUW1), and pBlueBac-derived vectors (such as the β -gal containing pBlueBac III).

10 When it is desirable to express only a portion of a myocilin protein, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from *E. coli* (Ben-Bassat et al. (1987) *J. Bacteriol.* 169:751-757) and *Salmonella typhimurium* and its *in vitro* activity has been demonstrated on recombinant proteins (Miller et al. (1987) *PNAS* 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either *in vivo* by expressing myocilin-derived polypeptides in a host which produces MAP (e.g., *E. coli* or CM89 or *S. cerevisiae*), or *in vitro* by use of purified MAP (e.g., procedure of Miller et al., *supra*).

20 In other embodiments transgenic animals, described in more detail below could be used to produce recombinant proteins.

4.4.2 Fusion proteins and Immunogens.

25 In another embodiment, the coding sequences for the polypeptide can be incorporated as a part of a fusion gene including a nucleotide sequence encoding a different polypeptide. This type of expression system can be useful under conditions where it is desirable to produce an immunogenic fragment of a myocilin protein. For example, the VP6 capsid protein of rotavirus can be used as an immunologic carrier protein for portions of the myocilin polypeptide, either in the monomeric form or in the form of a viral particle.

30 The nucleic acid sequences corresponding to the portion of a subject myocilin protein to which antibodies are to be raised can be incorporated into a fusion gene construct which includes coding sequences for a late vaccinia virus structural protein to produce a set of recombinant viruses expressing fusion proteins comprising myocilin epitopes as part of the virion. It has been demonstrated with the use of immunogenic fusion proteins utilizing the

Hepatitis B surface antigen fusion proteins that recombinant Hepatitis B virions can be utilized in this role as well. Similarly, chimeric constructs coding for fusion proteins containing a portion of a myocilin protein and the poliovirus capsid protein can be created to enhance immunogenicity of the set of polypeptide antigens (see, for example, EP
5 Publication No: 0259149; and Evans et al. (1989) *Nature* 339:385; Huang et al. (1988) *J. Virol.* 62:3855; and Schlienger et al. (1992) *J. Virol.* 66:2).

The Multiple Antigen Peptide system for peptide-based immunization can also be utilized to generate an immunogen, wherein a desired portion of a myocilin polypeptide is obtained directly from organo-chemical synthesis of the peptide onto an
10 oligomeric branching lysine core (see, for example, Posnett et al. (1988) *JBC* 263:1719 and Nardelli et al. (1992) *J. Immunol.* 148:914). Antigenic determinants of myocilin proteins can also be expressed and presented by bacterial cells.

In addition to utilizing fusion proteins to enhance immunogenicity, it is widely appreciated that fusion proteins can also facilitate the expression of proteins, and
15 accordingly, can be used in the expression of the myocilin polypeptides of the present invention. For example, myocilin polypeptides can be generated as glutathione-S-transferase (GST-fusion) proteins. Such GST-fusion proteins can enable easy purification of the myocilin polypeptide, as for example by the use of glutathione-derivatized matrices (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel et al. (N.Y.: John
20 Wiley & Sons, 1991)).

In another embodiment, a fusion gene coding for a purification leader sequence, such as a poly-(His)/enterokinase cleavage site sequence at the N-terminus of the desired portion of the recombinant protein, can allow purification of the expressed fusion protein by affinity chromatography using a Ni²⁺ metal resin. The purification leader
25 sequence can then be subsequently removed by treatment with enterokinase to provide the purified protein (e.g., see Hochuli et al. (1987) *J. Chromatography* 411:177; and Janknecht et al. *PNAS* 88:8972). Techniques for making fusion genes are known to those skilled in the art. Essentially, the joining of various DNA fragments coding for different polypeptide sequences is performed in accordance with conventional techniques, employing blunt-ended
30 or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers

which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel et al. John Wiley & Sons: 1992).

5

4.4.3. Antibodies

Another aspect of the invention pertains to an antibody or binding fragment thereof, which is specifically reactive with a myocilin protein. For example, by using immunogens derived from a myocilin protein, e.g. based on the cDNA sequences, anti-protein/anti-peptide antisera or monoclonal antibodies can be made by standard protocols (See, for example, *Antibodies: A Laboratory Manual* ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal, such as a mouse, a hamster or rabbit can be immunized with an immunogenic form of the peptide (e.g., a myocilin polypeptide or an antigenic fragment which is capable of eliciting an antibody response, or a fusion protein as described above). Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of a myocilin protein can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies. In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of a myocilin protein of a mammal, e.g. antigenic determinants of a protein represented by SEQ ID No: 2 or closely related homologs (e.g. at least 92% homologous, and more preferably at least 94% homologous).

Following immunization of an animal with an antigenic preparation of a myocilin polypeptide, anti-myocilin antisera can be obtained and, if desired, polyclonal anti-myocilin antibodies isolated from the serum. To produce monoclonal antibodies, antibody-producing cells (lymphocytes) can be harvested from an immunized animal and fused by standard somatic cell fusion procedures with immortalizing cells such as myeloma cells to yield hybridoma cells. Such techniques are well known in the art, and include, for example, the hybridoma technique (originally developed by Kohler and Milstein, (1975) *Nature*, 256: 495-497), the human B cell hybridoma technique (Kozbar et al., (1983) *Immunology Today*, 4: 72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., (1985) *Monoclonal Antibodies and Cancer*

Therapy, Alan R. Liss, Inc. pp. 77-96). Hybridoma cells can be screened immunochemically for production of antibodies specifically reactive with a myocilin polypeptide of the present invention and monoclonal antibodies isolated from a culture comprising such hybridoma cells.

5 The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with one of the subject mammalian myocilin polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, F(ab)₂ fragments can be generated by treating antibody with
10 pepsin. The resulting F(ab)₂ fragment can be treated to reduce disulfide bridges to produce Fab fragments. The antibody of the present invention is further intended to include bispecific and chimeric molecules having affinity for a myocilin protein conferred by at least one CDR region of the antibody.

 Antibodies which specifically bind myocilin epitopes can also be used in
15 immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of each of the subject myocilin polypeptides. Anti-myocilin antibodies can be used diagnostically in immuno-precipitation and immuno-blotting to detect and evaluate myocilin protein levels in tissue as part of a clinical testing procedure. For instance, such measurements can be useful in predictive valuations of
20 the onset or progression of proliferative disorders. Likewise, the ability to monitor myocilin protein levels in an individual can allow determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of myocilin polypeptides may be measured from cells in bodily fluid, such as in samples of cerebral spinal fluid or amniotic fluid, or can be measured in tissue, such as produced by
25 biopsy. Diagnostic assays using anti-myocilin antibodies can include, for example, immunoassays designed to aid in early diagnosis of a degenerative disorder, particularly ones which are manifest at birth. Diagnostic assays using anti-myocilin polypeptide antibodies can also include immunoassays designed to aid in early diagnosis and phenotyping neoplastic or hyperplastic disorders.

30 Another application of anti-myocilin antibodies of the present invention is in the immunological screening of cDNA libraries constructed in expression vectors such as gt11, gt18-23, ZAP, and ORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, gt11 will produce fusion proteins whose amino termini consist of β-

galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide. Antigenic epitopes of a myocilin protein, e.g. other orthologs of a particular myocilin protein or other paralogs from the same species, can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with
5 anti-myocilin antibodies. Positive phage detected by this assay can then be isolated from the infected plate. Thus, the presence of myocilin homologs can be detected and cloned from other animals, as can alternate isoforms (including splicing variants) from humans.

4.5 Transgenic animals

10 The invention further provides for transgenic animals, which can be used for a variety of purposes, e.g., to identify myocilin therapeutics. Transgenic animals of the invention include non-human animals containing a heterologous GLC1A gene or fragment thereof under the control of a GLC1A promoter or under the control of a heterologous promoter. Accordingly, the transgenic animals of the invention can be animals expressing
15 a transgene encoding a wild-type myocilin protein or fragment thereof or variants thereof, including mutants and polymorphic variants thereof. Such animals can be used, e.g., to determine the effect of a difference in amino acid sequence of a myocilin protein from the sequence set forth in SEQ ID NOS. 8 or 10, such as a polymorphic difference. These animals can also be used to determine the effect of expression of a myocilin protein in a
20 specific site or for identifying myocilin therapeutics or confirming their activity *in vivo*.

The transgenic animals can also be animals containing a transgene, such as reporter gene, under the control of a GLC1A promoter or fragment thereof. These animals are useful, e.g., for identifying drugs that modulate production of myocilin, such as by modulating GLC1A gene expression. A GLC1A gene promoter can be isolated, e.g., by
25 screening of a genomic library with a GLC1A cDNA fragment and characterized according to methods known in the art. In a preferred embodiment of the present invention, the transgenic animal containing said GLC1A reporter gene is used to screen a class of bioactive molecules known as steroid hormones for their ability to modulate GLC1A expression.

30 Yet other non-human animals within the scope of the invention include those in which the expression of the endogenous GLC1A gene has been mutated or "knocked out". A "knock out" animal is one carrying a homozygous or heterozygous deletion of a particular gene or genes. These animals could be used to determine whether the absence of GLC1A will result in a specific phenotype, in particular whether these mice have or are

likely to develop a specific disease, such as high susceptibility to heart disease or cancer. Furthermore these animals are useful in screens for drugs which alleviate or attenuate the disease condition resulting from the mutation of the GLC1A gene as outlined below. These animals are also useful for determining the effect of a specific amino acid difference, or allelic variation, in a GLC1A gene. That is, the GLC1A knock out animals can be crossed with transgenic animals expressing, e.g., a mutated form or allelic variant of GLC1A, thus resulting in an animal which expresses only the mutated protein and not the wild-type myocilin protein.

Methods for obtaining transgenic and knockout non-human animals are well known in the art. Knock out mice are generated by homologous integration of a "knock out" construct into a mouse embryonic stem cell chromosome which encodes the gene to be knocked out. In one embodiment, gene targeting, which is a method of using homologous recombination to modify an animal's genome, can be used to introduce changes into cultured embryonic stem cells. By targeting a GLC1A gene of interest in ES cells, these changes can be introduced into the germlines of animals to generate chimeras. The gene targeting procedure is accomplished by introducing into tissue culture cells a DNA targeting construct that includes a segment homologous to a target GLC1A locus, and which also includes an intended sequence modification to the GLC1A genomic sequence (e.g., insertion, deletion, point mutation). The treated cells are then screened for accurate targeting to identify and isolate those which have been properly targeted.

Gene targeting in embryonic stem cells is in fact a scheme contemplated by the present invention as a means for disrupting a GLC1A gene function through the use of a targeting transgene construct designed to undergo homologous recombination with one or more GLC1A genomic sequences. The targeting construct can be arranged so that, upon recombination with an element of a GLC1A gene, a positive selection marker is inserted into (or replaces) coding sequences of the gene. The inserted sequence functionally disrupts the GLC1A gene, while also providing a positive selection trait. Exemplary GLC1A targeting constructs are described in more detail below.

Generally, the embryonic stem cells (ES cells) used to produce the knockout animals will be of the same species as the knockout animal to be generated. Thus for example, mouse embryonic stem cells will usually be used for generation of knockout mice.

Embryonic stem cells are generated and maintained using methods well known to the skilled artisan such as those described by Doetschman et al. (1985) *J. Embryol. Exp.* 87:27-45). Any line of ES cells can be used, however, the line chosen is

typically selected for the ability of the cells to integrate into and become part of the germ line of a developing embryo so as to create germ line transmission of the knockout construct. Thus, any ES cell line that is believed to have this capability is suitable for use herein. One mouse strain that is typically used for production of ES cells, is the 129J strain.

5 Another ES cell line is murine cell line D3 (American Type Culture Collection, catalog no. CKL 1934) Still another preferred ES cell line is the WW6 cell line (Ioffe et al. (1995) *PNAS* 92:7357-7361). The cells are cultured and prepared for knockout construct insertion using methods well known to the skilled artisan, such as those set forth by Robertson in:
10 Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, E.J. Robertson, ed. IRL Press, Washington, D.C. [1987]); by Bradley et al. (1986) *Current Topics in Devel. Biol.* 20:357-371); and by Hogan et al. (Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY [1986]) .

A knock out construct refers to a uniquely configured fragment of nucleic acid which is introduced into a stem cell line and allowed to recombine with the genome
15 at the chromosomal locus of the gene of interest to be mutated. Thus a given knock out construct is specific for a given gene to be targeted for disruption. Nonetheless, many common elements exist among these constructs and these elements are well known in the art. A typical knock out construct contains nucleic acid fragments of not less than about 0.5 kb nor more than about 10.0 kb from both the 5' and the 3' ends of the genomic locus which
20 encodes the gene to be mutated. These two fragments are separated by an intervening fragment of nucleic acid which encodes a positive selectable marker, such as the neomycin resistance gene (neo^R). The resulting nucleic acid fragment, consisting of a nucleic acid from the extreme 5' end of the genomic locus linked to a nucleic acid encoding a positive selectable marker which is in turn linked to a nucleic acid from the extreme 3' end of the
25 genomic locus of interest, omits most of the coding sequence for GLC1A or other gene of interest to be knocked out. When the resulting construct recombines homologously with the chromosome at this locus, it results in the loss of the omitted coding sequence, otherwise known as the structural gene, from the genomic locus. A stem cell in which such a rare homologous recombination event has taken place can be selected for by virtue of the
30 stable integration into the genome of the nucleic acid of the gene encoding the positive selectable marker and subsequent selection for cells expressing this marker gene in the presence of an appropriate drug (neomycin in this example). Variations on this basic technique also exist and are well known in the art. For example, a "knock-in" construct refers to the same basic arrangement of a nucleic acid encoding a 5' genomic locus fragment

linked to nucleic acid encoding a positive selectable marker which in turn is linked to a nucleic acid encoding a 3' genomic locus fragment, but which differs in that none of the coding sequence is omitted and thus the 5' and the 3' genomic fragments used were initially contiguous before being disrupted by the introduction of the nucleic acid encoding the positive selectable marker gene. This "knock-in" type of construct is thus very useful for the construction of mutant transgenic animals when only a limited region of the genomic locus of the gene to be mutated, such as a single exon, is available for cloning and genetic manipulation. Alternatively, the "knock-in" construct can be used to specifically eliminate a single functional domain of the targeted gene, resulting in a transgenic animal which expresses a polypeptide of the targeted gene which is defective in one function, while retaining the function of other domains of the encoded polypeptide. This type of "knock-in" mutant frequently has the characteristic of a so-called "dominant negative" mutant because, especially in the case of proteins which homomultimerize, it can specifically block the action of (or "poison") the polypeptide product of the wild-type gene from which it was derived. In a variation of the knock-in technique, a marker gene is integrated at the genomic locus of interest such that expression of the marker gene comes under the control of the transcriptional regulatory elements of the targeted gene. A marker gene is one that encodes an enzyme whose activity can be detected (e.g., β -galactosidase), the enzyme substrate can be added to the cells under suitable conditions, and the enzymatic activity can be analyzed. One skilled in the art will be familiar with other useful markers and the means for detecting their presence in a given cell. All such markers are contemplated as being included within the scope of the teaching of this invention.

As mentioned above, the homologous recombination of the above described "knock out" and "knock in" constructs is very rare and frequently such a construct inserts nonhomologously into a random region of the genome where it has no effect on the gene which has been targeted for deletion, and where it can potentially recombine so as to disrupt another gene which was otherwise not intended to be altered. Such nonhomologous recombination events can be selected against by modifying the abovementioned knock out and knock in constructs so that they are flanked by negative selectable markers at either end (particularly through the use of two allelic variants of the thymidine kinase gene, the polypeptide product of which can be selected against in expressing cell lines in an appropriate tissue culture medium well known in the art - i.e. one containing a drug such as 5-bromodeoxyuridine). Thus a preferred embodiment of such a knock out or knock in construct of the invention consist of a nucleic acid encoding a negative selectable marker

linked to a nucleic acid encoding a 5' end of a genomic locus linked to a nucleic acid of a positive selectable marker which in turn is linked to a nucleic acid encoding a 3' end of the same genomic locus which in turn is linked to a second nucleic acid encoding a negative selectable marker. Nonhomologous recombination between the resulting knock out construct and the genome will usually result in the stable integration of one or both of these negative selectable marker genes and hence cells which have undergone nonhomologous recombination can be selected against by growth in the appropriate selective media (e.g. media containing a drug such as 5-bromodeoxyuridine for example). Simultaneous selection for the positive selectable marker and against the negative selectable marker will result in a vast enrichment for clones in which the knock out construct has recombined homologously at the locus of the gene intended to be mutated. The presence of the predicted chromosomal alteration at the targeted gene locus in the resulting knock out stem cell line can be confirmed by means of Southern blot analytical techniques which are well known to those familiar in the art. Alternatively, PCR can be used.

Each knockout construct to be inserted into the cell must first be in the linear form. Therefore, if the knockout construct has been inserted into a vector (described *infra*), linearization is accomplished by digesting the DNA with a suitable restriction endonuclease selected to cut only within the vector sequence and not within the knockout construct sequence.

For insertion, the knockout construct is added to the ES cells under appropriate conditions for the insertion method chosen, as is known to the skilled artisan. For example, if the ES cells are to be electroporated, the ES cells and knockout construct DNA are exposed to an electric pulse using an electroporation machine and following the manufacturer's guidelines for use. After electroporation, the ES cells are typically allowed to recover under suitable incubation conditions. The cells are then screened for the presence of the knock out construct as explained above. Where more than one construct is to be introduced into the ES cell, each knockout construct can be introduced simultaneously or one at a time.

After suitable ES cells containing the knockout construct in the proper location have been identified by the selection techniques outlined above, the cells can be inserted into an embryo. Insertion may be accomplished in a variety of ways known to the skilled artisan, however a preferred method is by microinjection. For microinjection, about 10-30 cells are collected into a micropipet and injected into embryos that are at the proper stage of development to permit integration of the foreign ES cell containing the knockout

construct into the developing embryo. For instance, the transformed ES cells can be microinjected into blastocytes. The suitable stage of development for the embryo used for insertion of ES cells is very species dependent, however for mice it is about 3.5 days. The embryos are obtained by perfusing the uterus of pregnant females. Suitable methods for accomplishing this are known to the skilled artisan, and are set forth by, e.g., Bradley et al. (supra).

While any embryo of the right stage of development is suitable for use, preferred embryos are male. In mice, the preferred embryos also have genes coding for a coat color that is different from the coat color encoded by the ES cell genes. In this way, the offspring can be screened easily for the presence of the knockout construct by looking for mosaic coat color (indicating that the ES cell was incorporated into the developing embryo). Thus, for example, if the ES cell line carries the genes for white fur, the embryo selected will carry genes for black or brown fur.

After the ES cell has been introduced into the embryo, the embryo may be implanted into the uterus of a pseudopregnant foster mother for gestation. While any foster mother may be used, the foster mother is typically selected for her ability to breed and reproduce well, and for her ability to care for the young. Such foster mothers are typically prepared by mating with vasectomized males of the same species. The stage of the pseudopregnant foster mother is important for successful implantation, and it is species dependent. For mice, this stage is about 2-3 days pseudopregnant.

Offspring that are born to the foster mother may be screened initially for mosaic coat color where the coat color selection strategy (as described above, and in the appended examples) has been employed. In addition, or as an alternative, DNA from tail tissue of the offspring may be screened for the presence of the knockout construct using Southern blots and/or PCR as described above. Offspring that appear to be mosaics may then be crossed to each other, if they are believed to carry the knockout construct in their germ line, in order to generate homozygous knockout animals. Homozygotes may be identified by Southern blotting of equivalent amounts of genomic DNA from mice that are the product of this cross, as well as mice that are known heterozygotes and wild type mice.

Other means of identifying and characterizing the knockout offspring are available. For example, Northern blots can be used to probe the mRNA for the presence or absence of transcripts encoding either the gene knocked out, the marker gene, or both. In addition, Western blots can be used to assess the level of expression of the GLC1A gene knocked out in various tissues of the offspring by probing the Western blot with an antibody

against the particular myocilin protein, or an antibody against the marker gene product, where this gene is expressed. Finally, *in situ* analysis (such as fixing the cells and labeling with antibody) and/or FACS (fluorescence activated cell sorting) analysis of various cells from the offspring can be conducted using suitable antibodies to look for the presence or
5 absence of the knockout construct gene product.

Yet other methods of making knock-out or disruption transgenic animals are also generally known. See, for example, *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Recombinase dependent knockouts can also be generated, e.g. by homologous recombination to insert target
10 sequences, such that tissue specific and/or temporal control of inactivation of a GLC1A-gene can be controlled by recombinase sequences (described *infra*).

Animals containing more than one knockout construct and/or more than one transgene expression construct are prepared in any of several ways. The preferred manner of preparation is to generate a series of mammals, each containing one of the desired
15 transgenic phenotypes. Such animals are bred together through a series of crosses, backcrosses and selections, to ultimately generate a single animal containing all desired knockout constructs and/or expression constructs, where the animal is otherwise congenic (genetically identical) to the wild type except for the presence of the knockout construct(s) and/or transgene(s).

A GLC1A transgene can encode the wild-type form of the protein, or can encode homologs thereof, including both agonists and antagonists, as well as antisense constructs. In preferred embodiments, the expression of the transgene is restricted to specific subsets of cells, tissues or developmental stages utilizing, for example, cis-acting
20 sequences that control expression in the desired pattern. In the present invention, such mosaic expression of a myocilin protein can be essential for many forms of lineage analysis and can additionally provide a means to assess the effects of, for example, lack of GLC1A expression which might grossly alter development in small patches of tissue within an otherwise normal embryo. Toward this end, tissue-specific regulatory sequences and conditional regulatory sequences can be used to control expression of the transgene in
25 certain spatial patterns. Moreover, temporal patterns of expression can be provided by, for example, conditional recombination systems or prokaryotic transcriptional regulatory sequences.

Genetic techniques, which allow for the expression of transgenes can be regulated via site-specific genetic manipulation *in vivo*, are known to those skilled in the art.

For instance, genetic systems are available which allow for the regulated expression of a recombinase that catalyzes the genetic recombination of a target sequence. As used herein, the phrase "target sequence" refers to a nucleotide sequence that is genetically recombined by a recombinase. The target sequence is flanked by recombinase recognition sequences and is generally either excised or inverted in cells expressing recombinase activity. Recombinase catalyzed recombination events can be designed such that recombination of the target sequence results in either the activation or repression of expression of one of the subject myocilin proteins. For example, excision of a target sequence which interferes with the expression of a recombinant GLC1A gene, such as one which encodes an antagonistic homolog or an antisense transcript, can be designed to activate expression of that gene. This interference with expression of the protein can result from a variety of mechanisms, such as spatial separation of the GLC1A gene from the promoter element or an internal stop codon. Moreover, the transgene can be made wherein the coding sequence of the gene is flanked by recombinase recognition sequences and is initially transfected into cells in a 3' to 5' orientation with respect to the promoter element. In such an instance, inversion of the target sequence will reorient the subject gene by placing the 5' end of the coding sequence in an orientation with respect to the promoter element which allow for promoter driven transcriptional activation.

The transgenic animals of the present invention all include within a plurality of their cells a transgene of the present invention, which transgene alters the phenotype of the "host cell" with respect to regulation of cell growth, death and/or differentiation. Since it is possible to produce transgenic organisms of the invention utilizing one or more of the transgene constructs described herein, a general description will be given of the production of transgenic organisms by referring generally to exogenous genetic material. This general description can be adapted by those skilled in the art in order to incorporate specific transgene sequences into organisms utilizing the methods and materials described below.

In an illustrative embodiment, either the *cre/loxP* recombinase system of bacteriophage P1 (Lakso et al. (1992) *PNAS* 89:6232-6236; Orban et al. (1992) *PNAS* 89:6861-6865) or the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman et al. (1991) *Science* 251:1351-1355; PCT publication WO 92/15694) can be used to generate *in vivo* site-specific genetic recombination systems. Cre recombinase catalyzes the site-specific recombination of an intervening target sequence located between *loxP* sequences. *loxP* sequences are 34 base pair nucleotide repeat sequences to which the Cre recombinase binds and are required for Cre recombinase mediated genetic recombination.

The orientation of *loxP* sequences determines whether the intervening target sequence is excised or inverted when Cre recombinase is present (Abremski et al. (1984) *J. Biol. Chem.* 259:1509-1514); catalyzing the excision of the target sequence when the *loxP* sequences are oriented as direct repeats and catalyzes inversion of the target sequence when *loxP* sequences are oriented as inverted repeats.

Accordingly, genetic recombination of the target sequence is dependent on expression of the Cre recombinase. Expression of the recombinase can be regulated by promoter elements which are subject to regulatory control, e.g., tissue-specific, developmental stage-specific, inducible or repressible by externally added agents. This regulated control will result in genetic recombination of the target sequence only in cells where recombinase expression is mediated by the promoter element. Thus, the activation expression of a recombinant myocilin protein can be regulated via control of recombinase expression.

Use of the *cre/loxP* recombinase system to regulate expression of a recombinant myocilin protein requires the construction of a transgenic animal containing transgenes encoding both the Cre recombinase and the subject protein. Animals containing both the Cre recombinase and a recombinant GLC1A gene can be provided through the construction of "double" transgenic animals. A convenient method for providing such animals is to mate two transgenic animals each containing a transgene, e.g., a GLC1A gene and recombinase gene.

Similar conditional transgenes can be provided using prokaryotic promoter sequences which require prokaryotic proteins to be simultaneously expressed in order to facilitate expression of the GLC1A transgene. Exemplary promoters and the corresponding trans-activating prokaryotic proteins are given in U.S. Patent No. 4,833,080.

Moreover, expression of the conditional transgenes can be induced by gene therapy-like methods wherein a gene encoding the trans-activating protein, e.g. a recombinase or a prokaryotic protein, is delivered to the tissue and caused to be expressed, such as in a cell-type specific manner. By this method, a GLC1A transgene could remain silent into adulthood until "turned on" by the introduction of the trans-activator.

In an exemplary embodiment, the "transgenic non-human animals" of the invention are produced by introducing transgenes into the germline of the non-human animal. Embryonal target cells at various developmental stages can be used to introduce transgenes. Different methods are used depending on the stage of development of the embryonal target cell. The specific line(s) of any animal used to practice this invention are

selected for general good health, good embryo yields, good pronuclear visibility in the embryo, and good reproductive fitness. In addition, the haplotype is a significant factor. For example, when transgenic mice are to be produced, strains such as C57BL/6 or FVB lines are often used (Jackson Laboratory, Bar Harbor, ME). Preferred strains are those with H-2^b, H-2^d or H-2^q haplotypes such as C57BL/6 or DBA/1. The line(s) used to practice this invention may themselves be transgenics, and/or may be knockouts (i.e., obtained from animals which have one or more genes partially or completely suppressed) .

In one embodiment, the transgene construct is introduced into a single stage embryo. The zygote is the best target for micro-injection. In the mouse, the male pronucleus reaches the size of approximately 20 micrometers in diameter which allows reproducible injection of 1-2pl of DNA solution. The use of zygotes as a target for gene transfer has a major advantage in that in most cases the injected DNA will be incorporated into the host gene before the first cleavage (Brinster et al. (1985) *PNAS* 82:4438-4442). As a consequence, all cells of the transgenic animal will carry the incorporated transgene. This will in general also be reflected in the efficient transmission of the transgene to offspring of the founder since 50% of the germ cells will harbor the transgene.

Normally, fertilized embryos are incubated in suitable media until the pronuclei appear. At about this time, the nucleotide sequence comprising the transgene is introduced into the female or male pronucleus as described below. In some species such as mice, the male pronucleus is preferred. It is most preferred that the exogenous genetic material be added to the male DNA complement of the zygote prior to its being processed by the ovum nucleus or the zygote female pronucleus. It is thought that the ovum nucleus or female pronucleus release molecules which affect the male DNA complement, perhaps by replacing the protamines of the male DNA with histones, thereby facilitating the combination of the female and male DNA complements to form the diploid zygote.

Thus, it is preferred that the exogenous genetic material be added to the male complement of DNA or any other complement of DNA prior to its being affected by the female pronucleus. For example, the exogenous genetic material is added to the early male pronucleus, as soon as possible after the formation of the male pronucleus, which is when the male and female pronuclei are well separated and both are located close to the cell membrane. Alternatively, the exogenous genetic material could be added to the nucleus of the sperm after it has been induced to undergo decondensation. Sperm containing the exogenous genetic material can then be added to the ovum or the decondensed sperm could

be added to the ovum with the transgene constructs being added as soon as possible thereafter.

Introduction of the transgene nucleotide sequence into the embryo may be accomplished by any means known in the art such as, for example, microinjection, electroporation, or lipofection. Following introduction of the transgene nucleotide sequence into the embryo, the embryo may be incubated *in vitro* for varying amounts of time, or reimplanted into the surrogate host, or both. In vitro incubation to maturity is within the scope of this invention. One common method is to incubate the embryos in vitro for about 1-7 days, depending on the species, and then reimplant them into the surrogate host.

For the purposes of this invention a zygote is essentially the formation of a diploid cell which is capable of developing into a complete organism. Generally, the zygote will be comprised of an egg containing a nucleus formed, either naturally or artificially, by the fusion of two haploid nuclei from a gamete or gametes. Thus, the gamete nuclei must be ones which are naturally compatible, i.e., ones which result in a viable zygote capable of undergoing differentiation and developing into a functioning organism. Generally, a euploid zygote is preferred. If an aneuploid zygote is obtained, then the number of chromosomes should not vary by more than one with respect to the euploid number of the organism from which either gamete originated.

In addition to similar biological considerations, physical ones also govern the amount (e.g., volume) of exogenous genetic material which can be added to the nucleus of the zygote or to the genetic material which forms a part of the zygote nucleus. If no genetic material is removed, then the amount of exogenous genetic material which can be added is limited by the amount which will be absorbed without being physically disruptive. Generally, the volume of exogenous genetic material inserted will not exceed about 10 picoliters. The physical effects of addition must not be so great as to physically destroy the viability of the zygote. The biological limit of the number and variety of DNA sequences will vary depending upon the particular zygote and functions of the exogenous genetic material and will be readily apparent to one skilled in the art, because the genetic material, including the exogenous genetic material, of the resulting zygote must be biologically capable of initiating and maintaining the differentiation and development of the zygote into a functional organism.

The number of copies of the transgene constructs which are added to the zygote is dependent upon the total amount of exogenous genetic material added and will be the amount which enables the genetic transformation to occur. Theoretically only one copy

is required; however, generally, numerous copies are utilized, for example, 1,000-20,000 copies of the transgene construct, in order to insure that one copy is functional. As regards the present invention, there will often be an advantage to having more than one functioning copy of each of the inserted exogenous DNA sequences to enhance the phenotypic expression of the exogenous DNA sequences.

Any technique which allows for the addition of the exogenous genetic material into nucleic genetic material can be utilized so long as it is not destructive to the cell, nuclear membrane or other existing cellular or genetic structures. The exogenous genetic material is preferentially inserted into the nucleic genetic material by microinjection. Microinjection of cells and cellular structures is known and is used in the art.

Reimplantation is accomplished using standard methods. Usually, the surrogate host is anesthetized, and the embryos are inserted into the oviduct. The number of embryos implanted into a particular host will vary by species, but will usually be comparable to the number of off spring the species naturally produces.

Transgenic offspring of the surrogate host may be screened for the presence and/or expression of the transgene by any suitable method. Screening is often accomplished by Southern blot or Northern blot analysis, using a probe that is complementary to at least a portion of the transgene. Western blot analysis using an antibody against the protein encoded by the transgene may be employed as an alternative or additional method for screening for the presence of the transgene product. Typically, DNA is prepared from tail tissue and analyzed by Southern analysis or PCR for the transgene. Alternatively, the tissues or cells believed to express the transgene at the highest levels are tested for the presence and expression of the transgene using Southern analysis or PCR, although any tissues or cell types may be used for this analysis.

Alternative or additional methods for evaluating the presence of the transgene include, without limitation, suitable biochemical assays such as enzyme and/or immunological assays, histological stains for particular marker or enzyme activities, flow cytometric analysis, and the like. Analysis of the blood may also be useful to detect the presence of the transgene product in the blood, as well as to evaluate the effect of the transgene on the levels of various types of blood cells and other blood constituents.

Progeny of the transgenic animals may be obtained by mating the transgenic animal with a suitable partner, or by *in vitro* fertilization of eggs and/or sperm obtained from the transgenic animal. Where mating with a partner is to be performed, the partner may or may not be transgenic and/or a knockout; where it is transgenic, it may contain the

same or a different transgene, or both. Alternatively, the partner may be a parental line. Where *in vitro* fertilization is used, the fertilized embryo may be implanted into a surrogate host or incubated *in vitro*, or both. Using either method, the progeny may be evaluated for the presence of the transgene using methods described above, or other appropriate methods.

5 The transgenic animals produced in accordance with the present invention will include exogenous genetic material. As set out above, the exogenous genetic material will, in certain embodiments, be a DNA sequence which results in the production of a myocilin protein (either agonistic or antagonistic), and antisense transcript, or a myocilin mutant. Further, in such embodiments the sequence will be attached to a transcriptional
10 control element, e.g., a promoter, which preferably allows the expression of the transgene product in a specific type of cell.

 Retroviral infection can also be used to introduce transgene into a non-human animal. The developing non-human embryo can be cultured *in vitro* to the blastocyst stage. During this time, the blastomeres can be targets for retroviral infection (Jaenich, R.
15 (1976) *PNAS* 73:1260-1264). Efficient infection of the blastomeres is obtained by enzymatic treatment to remove the zona pellucida (*Manipulating the Mouse Embryo*, Hogan eds. (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 1986). The viral vector system used to introduce the transgene is typically a replication-defective retrovirus carrying the transgene (Jahner et al. (1985) *PNAS* 82:6927-6931; Van der Putten et al.
20 (1985) *PNAS* 82:6148-6152). Transfection is easily and efficiently obtained by culturing the blastomeres on a monolayer of virus-producing cells (Van der Putten, *supra*; Stewart et al. (1987) *EMBO J.* 6:383-388). Alternatively, infection can be performed at a later stage. Virus or virus-producing cells can be injected into the blastocoele (Jahner et al. (1982) *Nature* 298:623-628). Most of the founders will be mosaic for the transgene since
25 incorporation occurs only in a subset of the cells which formed the transgenic non-human animal. Further, the founder may contain various retroviral insertions of the transgene at different positions in the genome which generally will segregate in the offspring. In addition, it is also possible to introduce transgenes into the germ line by intrauterine retroviral infection of the midgestation embryo (Jahner et al. (1982) *supra*).

30 A third type of target cell for transgene introduction is the embryonal stem cell (ES). ES cells are obtained from pre-implantation embryos cultured *in vitro* and fused with embryos (Evans et al. (1981) *Nature* 292:154-156; Bradley et al. (1984) *Nature* 309:255-258; Gossler et al. (1986) *PNAS* 83: 9065-9069; and Robertson et al. (1986) *Nature* 322:445-448). Transgenes can be efficiently introduced into the ES cells by DNA

transfection or by retrovirus-mediated transduction. Such transformed ES cells can thereafter be combined with blastocysts from a non-human animal. The ES cells thereafter colonize the embryo and contribute to the germ line of the resulting chimeric animal. For review see Jaenisch, R. (1988) *Science* 240:1468-1474.

5

4.6. Drug Screening Assays for GLC1A Therapeutics

Based on the discovery of the GLC1A gene and specific mutations in the gene that correlate with the existence of glaucoma, one of skill in the art is able to use any of a variety of standard assays to screen for drugs, which will interfere with or otherwise
10 prevent the development of glaucoma. By addressing the molecular basis of glaucoma, these agents are expected to be superior to existing therapies.

For example, identification of the precise phenotype associated with these mutations can be used to identify functionally important regions of the protein. These specific mutations can then be used in other experiments which will include
15 overexpression in cell lines and the creation of transgenic animals. Ideally, one could identify mutations which reproducibly cause glaucoma at very different times in the person's life and then be able to show that these mutations had similar differences of effect in a cellular expression system or a transgenic animal.

In addition, proteins that interact with the GLC1A gene product and
20 genes encoding the proteins can now be identified, since proteins that interact with GLC1A gene product will be important targets for involvement in the pathogenesis of various types of glaucoma.

Further, studies will be undertaken to discover whether mutations known to cause glaucoma in human beings alter protein trafficking in tissue culture as well as
25 animal models, since one mechanism through which mutations in the GLC1A gene could cause disease would be to alter the expression of other important gene products. This can occur by affecting overall protein trafficking within the cell caused for example by increased removal of mutant proteins at the level of the endoplasmic reticulum.

Further understanding of the pathogenesis of glaucoma is useful for
30 identifying new classes of drugs which can be useful in the treatment of glaucoma. For example, the GLC1A gene has been found to be induced by exposure of cells to steroids. Therefore, drugs which are capable of blocking this steroid effect should prove useful for preventing or delaying the development of glaucoma.

As further described below, *in vitro* assays which are suitable for very high throughput screening of compounds can be performed. As the simplest example of this approach, one could use antibodies to the GLC1A gene product to develop a simple ELISA assay for the induction of the GLC1A gene product and then perform this assay
5 in a 96 well microtiter plate format to screen a large number of drugs for the efficacy in blocking the steroid induction of the gene product. In this way, automated methods could be used to screen several thousand potentially therapeutic compounds for efficacy.

Also, knowledge of the structure/function of the GLC1A gene immediately suggests other genes which might be involved in glaucoma. Such clues
10 will come from studies of homology, evolution, evaluation of structural motifs within the gene, and genetic studies using analyses designed to identify genes causing polygenic disease.

In the original linkage study described herein, it was recognized that 3 of 22 obligate carriers of the glaucoma gene failed to manifest a severe glaucoma
15 phenotype. This information suggests that other genes are capable of mitigating the effect of the GLC1A mutation. One powerful way to search for such mitigator genes is to express a glaucoma-causing gene in different backgrounds. This can be done by creating transgenic animals and then breeding the glaucoma-causing gene on different genetic mouse strains. If the phenotype is altered in different strains these animals can
20 be back crossed in such a way that the mitigating gene can be identified.

Some of the assays mentioned above, will now be described in further detail below.

25 4.6.1 Cell-free assays

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins, are often preferred
30 as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an

alteration of binding affinity with upstream or downstream elements. Accordingly, in an exemplary screening assay of the present invention, the compound of interest is contacted with proteins which may function upstream (including both activators and repressors of its activity) or to proteins or nucleic acids which may function downstream of the myocilin polypeptide, whether they are positively or negatively regulated by it. To the mixture of the compound and the upstream or downstream element is then added a composition containing a myocilin polypeptide. Detection and quantification of complexes of myocilin with its upstream or downstream elements provide a means for determining a compound's efficacy at inhibiting (or potentiating) complex formation between myocilin and a myocilin-binding element. The efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. In the control assay, isolated and purified myocilin polypeptide is added to a composition containing the myocilin-binding element, and the formation of a complex is quantitated in the absence of the test compound.

Complex formation between the myocilin polypeptide and a myocilin binding element may be detected by a variety of techniques. Modulation of the formation of complexes can be quantitated using, for example, detectably labeled proteins such as radiolabeled, fluorescently labeled, or enzymatically labeled myocilin polypeptides, by immunoassay, or by chromatographic detection.

Typically, it will be desirable to immobilize either myocilin or its binding protein to facilitate separation of complexes from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of myocilin to an upstream or downstream element, in the presence and absence of a candidate agent, can be accomplished in any vessel suitable for containing the reactants. Examples include microtitre plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided which adds a domain that allows the protein to be bound to a matrix. For example, glutathione-S-transferase/myocilin (GST/myocilin) fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtitre plates, which are then combined with the cell lysates, e.g. an ^{35}S -labeled, and the test compound, and the mixture incubated under conditions conducive to complex formation, e.g. at physiological conditions for salt and pH, though slightly more stringent conditions may be desired. Following incubation, the beads are washed to remove any unbound label, and the matrix immobilized and radiolabel

determined directly (e.g. beads placed in scintillant), or in the supernatant after the complexes are subsequently dissociated. Alternatively, the complexes can be dissociated from the matrix, separated by SDS-PAGE, and the level of myocilin-binding protein found in the bead fraction quantitated from the gel using standard electrophoretic techniques such as described in the appended examples.

Other techniques for immobilizing proteins on matrices are also available for use in the subject assay. For instance, either myocilin or its cognate binding protein can be immobilized utilizing conjugation of biotin and streptavidin. For instance, biotinylated myocilin molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with myocilin but which do not interfere with binding of upstream or downstream elements can be derivatized to the wells of the plate, and myocilin trapped in the wells by antibody conjugation. As above, preparations of a myocilin-binding protein and a test compound are incubated in the myocilin-presenting wells of the plate, and the amount of complex trapped in the well can be quantitated. Exemplary methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the myocilin binding element, or which are reactive with myocilin protein and compete with the binding element; as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the binding element, either intrinsic or extrinsic activity. In the instance of the latter, the enzyme can be chemically conjugated or provided as a fusion protein with the myocilin-BP. To illustrate, the myocilin-BP can be chemically cross-linked or genetically fused with horseradish peroxidase, and the amount of polypeptide trapped in the complex can be assessed with a chromogenic substrate of the enzyme, e.g. 3,3'-diamino-benzadine tetrahydrochloride or 4-chloro-1-naphthol. Likewise, a fusion protein comprising the polypeptide and glutathione-S-transferase can be provided, and complex formation quantitated by detecting the GST activity using 1-chloro-2,4-dinitrobenzene (Habig et al (1974) J Biol Chem 249:7130).

For processes which rely on immunodetection for quantitating one of the proteins trapped in the complex, antibodies against the protein, such as anti-myocilin antibodies, can be used. Alternatively, the protein to be detected in the complex can be "epitope tagged" in the form of a fusion protein which includes, in addition to the myocilin sequence, a second polypeptide for which antibodies are readily available (e.g. from

commercial sources). For instance, the GST fusion proteins described above can also be used for quantification of binding using antibodies against the GST moiety. Other useful epitope tags include myc-epitopes (e.g., see Ellison et al. (1991) J Biol Chem 266:21150-21157) which includes a 10-residue sequence from c-myc, as well as the pFLAG system (International Biotechnologies, Inc.) or the pEZZ-protein A system (Pharmacia, NJ).

4.6.2. Cell based assays

In addition to cell-free assays, such as described above, the readily available source of mutant and functional GLC1A nucleic acids and proteins provided by the present invention also facilitates the generation of cell-based assays for identifying small molecule agonists/antagonists and the like. For example, cells can be caused to overexpress a recombinant myocilin protein in the presence and absence of a test agent of interest, with the assay scoring for modulation in myocilin responses by the target cell mediated by the test agent. As with the cell-free assays, agents which produce a statistically significant change in myocilin-dependent responses (either inhibition or potentiation) can be identified. In an illustrative embodiment, the expression or activity of a myocilin is modulated in cells and the effects of compounds of interest on the readout of interest (such as tissue differentiation, proliferation, tumorigenesis) are measured. For example, the expression of genes which are up- or down-regulated in response to a myocilin-dependent signal cascade can be assayed. In preferred embodiments, the regulatory regions of such genes, e.g., the 5' flanking promoter and enhancer regions, are operably linked to a detectable marker (such as luciferase) which encodes a gene product that can be readily detected.

Exemplary cells or cell lines may be derived from ocular tissue (e.g. trabecular meshwork or ciliary body epithelia); as well as generic mammalian cell lines such as HeLa cells and COS cells, e.g., COS-7 (ATCC# CRL-1651). Further, the transgenic animals discussed herein may be used to generate cell lines containing one or more cell types involved in glaucoma, that can be used as cell culture models for this disorder. While primary cultures derived from the glaucomatous transgenic animals of the invention may be utilized, the generation of continuous cell lines is preferred. For examples of techniques which may be used to derive a continuous cell line from the transgenic animals, see Small et al., 1985, Mol. Cell Biol. 5:642-648.

Using these cells, the effect of a test compound on a variety of end points can be tested including cell proliferation, migration, phagocytosis, adherence and/or biosynthesis (e.g. of extracellular matrix components). The cells can then be examined for

phenotypes associated with glaucoma, including, but not limited to changes in cellular morphology, cell proliferation, cell migration, and cell adhesion.

In the event that the myocilin proteins themselves, or in complexes with other proteins, are capable of binding DNA and modifying transcription of a gene, a transcriptional based assay could be used, for example, in which a myocilin responsive regulatory sequence is operably linked to a detectable marker gene.

Monitoring the influence of compounds on cells may be applied not only in basic drug screening, but also in clinical trials. In such clinical trials, the expression of a panel of genes may be used as a "read out" of a particular drug's therapeutic effect.

In yet another aspect of the invention, the subject myocilin polypeptides can be used to generate a "two hybrid" assay (see, for example, U.S. Patent No. 5,283,317; Zervos et al. (1993) Cell 72:223-232; Madura et al. (1993) J Biol Chem 268:12046-12054; Bartel et al. (1993) Biotechniques 14:920-924; Iwabuchi et al. (1993) Oncogene 8:1693-1696; and Brent WO94/10300), for isolating coding sequences for other cellular proteins which bind to or interact with myocilin ("myocilin-binding proteins" or "myocilin-bp).

Briefly, the two hybrid assay relies on reconstituting *in vivo* a functional transcriptional activator protein from two separate fusion proteins. In particular, the method makes use of chimeric genes which express hybrid proteins. To illustrate, a first hybrid gene comprises the coding sequence for a DNA-binding domain of a transcriptional activator fused in frame to the coding sequence for a myocilin polypeptide. The second hybrid protein encodes a transcriptional activation domain fused in frame to a sample gene from a cDNA library. If the bait and sample hybrid proteins are able to interact, e.g., form a myocilin-dependent complex, they bring into close proximity the two domains of the transcriptional activator. This proximity is sufficient to cause transcription of a reporter gene which is operably linked to a transcriptional regulatory site responsive to the transcriptional activator, and expression of the reporter gene can be detected and used to score for the interaction of the myocilin and sample proteins.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

4.7 Methods of Treating Disease

In addition to glaucoma, there may be a variety of pathological conditions for which myocilin therapeutics of the present invention can be used in treatment.

A "myocilin therapeutic," whether an antagonist or agonist of wild type myocilin, can be, as appropriate, any of the preparations described above, including isolated polypeptides, gene therapy constructs, antisense molecules, peptidomimetics, non-nucleic acid, non-peptidic small molecules, or agents identified in the drug assays provided herein.

5 As described herein, subjects having certain mutant GLC1A genes tend to develop glaucoma. Down-regulation of mutant GLC1A gene expression and/or a resultant decrease in the activity of a mutant myocilin protein (e.g. using antisense, ribozyme, triple helix or antibody molecules) and/or up-regulation of a wildtype GLC1A gene expression and/or a resultant increase in the activity of a wildtype myocilin protein (e.g. using gene
10 therapy or protein replacement therapies) should therefore prove useful in ameliorating disease symptoms. Compounds identified as increasing or decreasing GLC1A gene expression or myocilin protein activity can be administered to a subject at therapeutically effective dose to treat or ameliorate symptoms associated with glaucoma.

15 4.7.1. Effective Dose

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and
20 therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Compounds which exhibit large therapeutic indices are preferred. While compounds that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

25 The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method
30 of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC₅₀ (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such

information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

4.7.2. Formulation and Use

5 Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients. Thus, the compounds and their physiologically acceptable salts and solvates may be formulated for administration by, for example, injection, inhalation or insufflation (either through the mouth or the nose) or oral, buccal, parenteral
10 or rectal administration.

For such therapy, the oligomers of the invention can be formulated for a variety of loads of administration, including systemic and topical or localized administration. Techniques and formulations generally may be found in *Remington's Pharmaceutical Sciences*, Meade Publishing Co., Easton, PA. For systemic administration,
15 injection is preferred, including intramuscular, intravenous, intraperitoneal, and subcutaneous. For injection, the oligomers of the invention can be formulated in liquid solutions, preferably in physiologically compatible buffers such as Hank's solution or Ringer's solution. In addition, the oligomers may be formulated in solid form and redissolved or suspended immediately prior to use. Lyophilized forms are also included.

20 For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (*e.g.*, pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (*e.g.*, lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (*e.g.*, magnesium
25 stearate, talc or silica); disintegrants (*e.g.*, potato starch or sodium starch glycolate); or wetting agents (*e.g.*, sodium lauryl sulphate). The tablets may be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may
30 be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (*e.g.*, sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (*e.g.*, lecithin or acacia); non-aqueous vehicles (*e.g.*, almond oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (*e.g.*, methyl or

propyl-p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate.

Preparations for oral administration may be suitably formulated to give controlled release of the active compound.

5 For buccal administration the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*,
10 dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of *e.g.* gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

15 The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampoules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as
20 suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as
25 cocoa butter or other glycerides.

In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with
30 suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be

permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration bile salts and fusidic acid derivatives. In addition, detergents may be used to facilitate permeation. Transmucosal administration may be through nasal sprays or using suppositories. For topical administration, the
5 oligomers of the invention are formulated into ointments, salves, gels, or creams as generally known in the art.

In clinical settings, the gene delivery systems for the therapeutic GLC1A gene can be introduced into a patient by any of a number of methods, each of which is familiar in the art. For instance, a pharmaceutical preparation of the gene delivery system
10 can be introduced systemically, e.g. by intravenous injection, and specific transduction of the protein in the target cells occurs predominantly from specificity of transfection provided by the gene delivery vehicle, cell-type or tissue-type expression due to the transcriptional regulatory sequences controlling expression of the receptor gene, or a combination thereof. In other embodiments, initial delivery of the recombinant gene is more limited with
15 introduction into the animal being quite localized. For example, the gene delivery vehicle can be introduced by catheter (see U.S. Patent 5,328,470) or by stereotactic injection (e.g. Chen et al. (1994) *PNAS* 91: 3054-3057). A GLC1A gene, such as any one of the sequences represented in the group consisting of SEQ ID NO: 1 or 2, or a sequence homologous thereto can be delivered in a gene therapy construct by electroporation using techniques
20 described, for example, by Dev et al. ((1994) *Cancer Treat Rev* 20:105-115). Gene therapy vectors comprised of viruses that provide specific effective and highly localized treatment of eye diseases are described in Published International Patent Application No. WO 95/34580 to U. Eriksson et al..

The pharmaceutical preparation of the gene therapy construct can consist
25 essentially of the gene delivery system in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery system can be produced intact from recombinant cells, e.g. retroviral vectors, the pharmaceutical preparation can comprise one or more cells which produce the gene delivery system.

30 The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

4.8 Predictive Medicine

The invention further features predictive medicines, which are based, at least in part, on the identity of the novel GLC1A genes and alterations in the genes and related pathway genes, which affect the expression level and/or function of the encoded myocilin protein in a subject.

For example, information obtained using the diagnostic assays described herein (alone or in conjunction with information on another genetic defect, which contributes to the same disease) is useful for diagnosing or confirming that a symptomatic subject (e.g. a subject symptomatic for glaucoma), has a genetic defect (e.g. in a GLC1A gene or in a gene that regulates the expression of an GLC1A gene), which causes or contributes to glaucoma. Alternatively, the information (alone or in conjunction with information on another genetic defect, which contributes to the same disease) can be used prognostically for predicting whether a non-symptomatic subject is likely to develop glaucoma. Based on the prognostic information, a doctor can recommend a regimen or therapeutic protocol, useful for preventing or prolonging onset of glaucoma in the individual.

In addition, knowledge of the particular alteration or alterations resulting in defective or deficient GLC1A genes or proteins in an individual (the GLC1A genetic profile), alone or in conjunction with information on other genetic defects contributing to glaucoma (the genetic profile of glaucoma) allows customization of therapy to the individual's genetic profile, the goal of "pharmacogenomics". For example, an individual's GLC1A genetic profile or the genetic profile of glaucoma, can enable a doctor to: 1) more effectively prescribe a drug that will address the molecular basis of glaucoma; and 2) better determine the appropriate dosage of a particular drug. For example, the expression level of myocilin proteins, alone or in conjunction with the expression level of other genes, known to contribute to glaucoma, can be measured in many patients at various stages of the disease to generate a transcriptional or expression profile of glaucoma. Expression patterns of individual patients can then be compared to the expression profile of glaucoma to determine the appropriate drug and dose to administer to the patient.

The ability to target populations expected to show the highest clinical benefit, based on the GLC1A or glaucoma genetic profile, can enable: 1) the repositioning of marketed drugs with disappointing market results; 2) the rescue of drug candidates whose clinical development has been discontinued as a result of safety or efficacy limitations, which are patient subgroup-specific; and 3) an accelerated and less costly development for

drug candidates and more optimal drug labeling (e.g. since the use of GLC1A as a marker is useful for optimizing effective dose).

These and other methods are described in further detail in the following sections.

5

4.8.1. Prognostic and Diagnostic Assays

The present methods provide means for determining if a subject has (diagnostic) or is at risk of developing (prognostic) glaucoma.

In one embodiment, the method comprises determining whether a subject has
10 an abnormal GLC1A mRNA and/or myocilin protein level, such as by Northern blot analysis, reverse transcription-polymerase chain reaction (RT-PCR), *in situ* hybridization, immunoprecipitation, Western blot hybridization, or immunohistochemistry. According to the method, cells are obtained from a subject and the level of GLC1A mRNA or myocilin level is determined and compared to the mRNA or protein level in a healthy subject. An
15 abnormal level of GLC1A mRNA or myocilin therefor being indicative of an aberrant myocilin bioactivity.

In another embodiment, the method comprises measuring at least one activity of myocilin. Similarly, the constant of affinity of a myocilin protein of a subject with a binding partner can be determined. Comparison of the results obtained with results from
20 similar analysis performed on myocilin proteins from healthy subjects is indicative of whether a subject has an abnormal myocilin activity.

In preferred embodiments, the methods for determining whether a subject has or is at risk for developing glaucoma is characterized as comprising detecting, in a sample of cells from the subject, the presence or absence of a genetic alteration
25 characterized by at least one of (i) an alteration affecting the integrity of a gene encoding a myocilin polypeptide, or (ii) the mis-expression of the GLC1A gene. For example, such genetic alterations can be detected by ascertaining the existence of at least one of (i) a deletion of one or more nucleotides from a GLC1A gene, (ii) an addition of one or more nucleotides to a GLC1A gene, (iii) a substitution of one or more nucleotides of a GLC1A
30 gene, (iv) a gross chromosomal rearrangement of a GLC1A gene, (v) a gross alteration in the level of a messenger RNA transcript of a GLC1A gene, (vi) aberrant modification of a GLC1A gene, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a GLC1A gene, (viii) a non-wild type level of a myocilin polypeptide, (ix) allelic loss of a GLC1A gene, and/or

(x) inappropriate post-translational modification of a myocilin polypeptide. As set out below, the present invention provides a variety of assay techniques for detecting alterations in a GLC1A gene. These methods include, but are not limited to, methods involving sequence analysis, Southern blot hybridization, restriction enzyme site mapping, and methods involving detection of absence of nucleotide pairing between the nucleic acid to be analyzed and a probe. These and other methods are further described *infra*.

Specific diseases or disorders, e.g., genetic diseases or disorders, are associated with specific allelic variants of polymorphic regions of certain genes, which do not necessarily encode a mutated protein. Thus, the presence of a specific allelic variant of a polymorphic region of a gene, such as a single nucleotide polymorphism ("SNP"), in a subject can render the subject susceptible to developing a specific disease or disorder. Polymorphic regions in GLC1A genes, can be identified by determining the nucleotide sequence of genes in populations of individuals. If a polymorphic region, e.g., SNP is identified, then the link with a specific disease can be determined by studying specific populations of individuals, e.g., individuals which developed glaucoma. A polymorphic region can be located in any region of a gene, e.g., exons, in coding or non-coding regions of exons, introns, and promoter region.

It is likely that GLC1A genes comprise polymorphic regions, specific alleles of which may be associated with specific diseases or conditions or with an increased likelihood of developing such diseases or conditions. Thus, the invention provides methods for determining the identity of the allele or allelic variant of a polymorphic region of a GLC1A gene in a subject, to thereby determine whether the subject has or is at risk of developing a disease or disorder associated with a specific allelic variant of a polymorphic region.

In an exemplary embodiment, there is provided a nucleic acid composition comprising a nucleic acid probe including a region of nucleotide sequence which is capable of hybridizing to a sense or antisense sequence of a GLC1A gene or naturally occurring mutants thereof, or 5' or 3' flanking sequences or intronic sequences naturally associated with the subject GLC1A genes or naturally occurring mutants thereof. The nucleic acid of a cell is rendered accessible for hybridization, the probe is contacted with the nucleic acid of the sample, and the hybridization of the probe to the sample nucleic acid is detected. Such techniques can be used to detect alterations or allelic variants at either the genomic or mRNA level, including deletions, substitutions, etc., as well as to determine mRNA transcript levels.

A preferred detection method is allele specific hybridization using probes overlapping the mutation or polymorphic site and having about 5, 10, 20, 25, or 30 nucleotides around the mutation or polymorphic region. In a preferred embodiment of the invention, several probes capable of hybridizing specifically to allelic variants, such as single nucleotide polymorphisms, are attached to a solid phase support, e.g., a "chip". Oligonucleotides can be bound to a solid support by a variety of processes, including lithography. For example a chip can hold up to 250,000 oligonucleotides. Mutation detection analysis using these chips comprising oligonucleotides, also termed "DNA probe arrays" is described e.g., in Cronin et al. (1996) *Human Mutation* 7:244. In one embodiment, a chip comprises all the allelic variants of at least one polymorphic region of a gene. The solid phase support is then contacted with a test nucleic acid and hybridization to the specific probes is detected. Accordingly, the identity of numerous allelic variants of one or more genes can be identified in a simple hybridization experiment.

In certain embodiments, detection of the alteration comprises utilizing the probe/primer in a polymerase chain reaction (PCR) (see, e.g. U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligase chain reaction (LCR) (see, e.g., Landegran et al. (1988) *Science* 241:1077-1080; and Nakazawa et al. (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the GLC1A gene (see Abravaya et al. (1995) *Nuc Acid Res* 23:675-682). In a merely illustrative embodiment, the method includes the steps of (i) collecting a sample of cells from a patient, (ii) isolating nucleic acid (e.g., genomic, mRNA or both) from the cells of the sample, (iii) contacting the nucleic acid sample with one or more primers which specifically hybridize to a GLC1A gene under conditions such that hybridization and amplification of the GLC1A gene (if present) occurs, and (iv) detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli, J.C. et al., 1990, *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh, D.Y. et al., 1989, *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi, P.M. et al., 1988, *Bio/Technology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes

are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In a preferred embodiment of the subject assay, mutations in, or allelic variants, of a GLC1A gene from a sample cell are identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Patent No. 5,498,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the GLC1A gene and detect mutations by comparing the sequence of the sample GLC1A with the corresponding wild-type (control) sequence. Exemplary sequencing reactions include those based on techniques developed by Maxim and Gilbert (*Proc. Natl Acad Sci USA* (1977) 74:560) or Sanger (Sanger et al (1977) *Proc. Nat. Acad. Sci* 74:5463). It is also contemplated that any of a variety of automated sequencing procedures may be utilized when performing the subject assays (*Biotechniques* (1995) 19:448), including sequencing by mass spectrometry (see, for example PCT publication WO 94/16101; Cohen et al. (1996) *Adv Chromatogr* 36:127-162; and Griffin et al. (1993) *Appl Biochem Biotechnol* 38:147-159). It will be evident to one skilled in the art that, for certain embodiments, the occurrence of only one, two or three of the nucleic acid bases need be determined in the sequencing reaction. For instance, A-track or the like, e.g., where only one nucleic acid is detected, can be carried out.

In a further embodiment, protection from cleavage agents (such as a nuclease, hydroxylamine or osmium tetroxide and with piperidine) can be used to detect mismatched bases in RNA/RNA or RNA/DNA or DNA/DNA heteroduplexes (Myers, et al. (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes formed by hybridizing (labelled) RNA or DNA containing the wild-type GLC1A sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent which cleaves single-stranded regions of the duplex as will exist due to base pair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digest the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched

regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton et al (1988) *Proc. Natl Acad Sci USA* 85:4397; Saleeba et al (1992) *Methods Enzymol.* 217:286-295. In a preferred embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in GLC1A cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu et al. (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a GLC1A sequence, e.g., a wild-type GLC1A sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Patent No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations or the identity of the allelic variant of a polymorphic region in GLC1A genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita et al. (1989) *Proc Natl. Acad. Sci USA* 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; and Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments of sample and control GLC1A nucleic acids are denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In a preferred embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen et al. (1991) *Trends Genet* 7:5).

In yet another embodiment, the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE) (Myers et al (1985) *Nature* 313:495). When DGGE

is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing agent gradient to identify differences in the mobility of control and sample DNA (Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753).

Examples of other techniques for detecting point mutations or the identity of the allelic variant of a polymorphic region include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation or nucleotide difference (e.g., in allelic variants) is placed centrally and then hybridized to target DNA under conditions which permit hybridization only if a perfect match is found (Saiki et al. (1986) *Nature* 324:163); Saiki et al (1989) *Proc. Natl Acad. Sci USA* 86:6230). Such allele specific oligonucleotide hybridization techniques may be used to test one mutation or polymorphic region per reaction when oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations or polymorphic regions when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology which depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation or polymorphic region of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs et al (1989) *Nucleic Acids Res.* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238. In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection (Gasparini et al (1992) *Mol. Cell Probes* 6:1). It is anticipated that in certain embodiments amplification may also be performed using Taq ligase for amplification (Barany (1991) *Proc. Natl. Acad. Sci USA* 88:189). In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

In another embodiment, identification of the allelic variant is carried out using an oligonucleotide ligation assay (OLA), as described, e.g., in U.S. Pat. No. 4,998,617 and in Landegren, U. et al., *Science* 241:1077-1080 (1988). The OLA protocol uses two

oligonucleotides which are designed to be capable of hybridizing to abutting sequences of a single strand of a target. One of the oligonucleotides is linked to a separation marker, e.g., biotinylated, and the other is detectably labeled. If the precise complementary sequence is found in a target molecule, the oligonucleotides will hybridize such that their termini abut, and create a ligation substrate. Ligation then permits the labeled oligonucleotide to be recovered using avidin, or another biotin ligand. Nickerson, D. A. et al. have described a nucleic acid detection assay that combines attributes of PCR and OLA (Nickerson, D. A. et al., Proc. Natl. Acad. Sci. (U.S.A.) 87:8923-8927 (1990). In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA.

Several techniques based on this OLA method have been developed and can be used to detect specific allelic variants of a polymorphic region of a GLC1A gene. For example, U.S. Patent No. 5,593,826 discloses an OLA using an oligonucleotide having 3'-amino group and a 5'-phosphorylated oligonucleotide to form a conjugate having a phosphoramidate linkage. In another variation of OLA described in Tobe et al. ((1996) Nucleic Acids Res 24: 3728), OLA combined with PCR permits typing of two alleles in a single microtiter well. By marking each of the allele-specific primers with a unique hapten, i.e. digoxigenin and fluorescein, each OLA reaction can be detected by using hapten specific antibodies that are labeled with different enzyme reporters, alkaline phosphatase or horseradish peroxidase. This system permits the detection of the two alleles using a high throughput format that leads to the production of two different colors.

The invention further provides methods for detecting single nucleotide polymorphisms in a GLC1A gene. Because single nucleotide polymorphisms constitute sites of variation flanked by regions of invariant sequence, their analysis requires no more than the determination of the identity of the single nucleotide present at the site of variation and it is unnecessary to determine a complete gene sequence for each patient. Several methods have been developed to facilitate the analysis of such single nucleotide polymorphisms.

In one embodiment, the single base polymorphism can be detected by using a specialized exonuclease-resistant nucleotide, as disclosed, e.g., in Mundy, C. R. (U.S. Pat. No.4,656,127). According to the method, a primer complementary to the allelic sequence immediately 3' to the polymorphic site is permitted to hybridize to a target molecule obtained from a particular animal or human. If the polymorphic site on the target molecule contains a nucleotide that is complementary to the particular exonuclease-resistant nucleotide derivative present, then that derivative will be incorporated onto the end of the

hybridized primer. Such incorporation renders the primer resistant to exonuclease, and thereby permits its detection. Since the identity of the exonuclease-resistant derivative of the sample is known, a finding that the primer has become resistant to exonucleases reveals that the nucleotide present in the polymorphic site of the target molecule was
5 complementary to that of the nucleotide derivative used in the reaction. This method is advantageous, since it does not require the determination of large amounts of extraneous sequence data.

In another embodiment of the invention, a solution-based method is used for determining the identity of the nucleotide of a polymorphic site. Cohen, D. et al. (French
10 Patent 2,650,840; PCT Appln. No. WO91/02087). As in the Mundy method of U.S. Pat. No. 4,656,127, a primer is employed that is complementary to allelic sequences immediately 3' to a polymorphic site. The method determines the identity of the nucleotide of that site using labeled dideoxynucleotide derivatives, which, if complementary to the nucleotide of the polymorphic site will become incorporated onto the terminus of the
15 primer.

An alternative method, known as Genetic Bit Analysis or GBA TM is described by Goelet, P. et al. (PCT Appln. No. 92/15712). The method of Goelet, P. et al. uses mixtures of labeled terminators and a primer that is complementary to the sequence 3' to a polymorphic site. The labeled terminator that is incorporated is thus determined by, and
20 complementary to, the nucleotide present in the polymorphic site of the target molecule being evaluated. In contrast to the method of Cohen et al. (French Patent 2,650,840; PCT Appln. No. WO91/02087) the method of Goelet, P. et al. is preferably a heterogeneous phase assay, in which the primer or the target molecule is immobilized to a solid phase.

Recently, several primer-guided nucleotide incorporation procedures for
25 assaying polymorphic sites in DNA have been described (Komher, J. S. et al., Nucl. Acids. Res. 17:7779-7784 (1989); Sokolov, B. P., Nucl. Acids Res. 18:3671 (1990); Syvanen, A. -C., et al., Genomics 8:684-692 (1990); Kuppuswamy, M. N. et al., Proc. Natl. Acad. Sci. (U.S.A.) 88:1143-1147 (1991); Prezant, T. R. et al., Hum. Mutat. 1:159-164 (1992); Ugozzoli, L. et al., GATA 9:107-112 (1992); Nyren, P. et al., Anal. Biochem. 208:171-175
30 (1993)). These methods differ from GBA TM in that they all rely on the incorporation of labeled deoxynucleotides to discriminate between bases at a polymorphic site. In such a format, since the signal is proportional to the number of deoxynucleotides incorporated, polymorphisms that occur in runs of the same nucleotide can result in signals that are

proportional to the length of the run (Syvanen, A. -C., et al., *Amer.J. Hum. Genet.* 52:46-59 (1993)).

For mutations that produce premature termination of protein translation, the protein truncation test (PTT) offers an efficient diagnostic approach (Roest, et. al., (1993) *Hum. Mol. Genet.* 2:1719-21; van der Lijst, et. al., (1994) *Genomics* 20:1-4). For PTT, RNA is initially isolated from available tissue and reverse-transcribed, and the segment of interest is amplified by PCR. The products of reverse transcription PCR are then used as a template for nested PCR amplification with a primer that contains an RNA polymerase promoter and a sequence for initiating eukaryotic translation. After amplification of the region of interest, the unique motifs incorporated into the primer permit sequential *in vitro* transcription and translation of the PCR products. Upon sodium dodecyl sulfate-polyacrylamide gel electrophoresis of translation products, the appearance of truncated polypeptides signals the presence of a mutation that causes premature termination of translation. In a variation of this technique, DNA (as opposed to RNA) is used as a PCR template when the target region of interest is derived from a single exon.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid, primer set; and/or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of glaucoma.

Any cell type or tissue may be utilized in the diagnostics described below. In a preferred embodiment a bodily fluid, *e.g.*, blood, is obtained from the subject to determine the presence of a mutation or the identity of the allelic variant of a polymorphic region of a GLC1A gene. A bodily fluid, *e.g.*, blood, can be obtained by known techniques (*e.g.* venipuncture). Alternatively, nucleic acid tests can be performed on dry samples (*e.g.* hair or skin). For prenatal diagnosis, fetal nucleic acid samples can be obtained from maternal blood as described in International Patent Application No. WO91/07660 to Bianchi. Alternatively, amniocytes or chorionic villi may be obtained for performing prenatal testing.

When using RNA or protein to determine the presence of a mutation or of a specific allelic variant of a polymorphic region of a GLC1A gene, the cells or tissues that may be utilized must express the GLC1A gene. Preferred cells for use in these methods include photoreceptors cells of retina. Alternative cells or tissues that can be used, can be identified by determining the expression pattern of the specific GLC1A gene in a subject, such as by Northern blot analysis.

Diagnostic procedures may also be performed *in situ* directly upon tissue sections (fixed and/or frozen) of patient tissue obtained from biopsies or resections, such that no nucleic acid purification is necessary. Nucleic acid reagents may be used as probes and/or primers for such *in situ* procedures (see, for example, Nuovo, G.J., 1992, PCR *in situ* hybridization: protocols and applications, Raven Press, NY).

In addition to methods which focus primarily on the detection of one nucleic acid sequence, profiles may also be assessed in such detection schemes. Fingerprint profiles may be generated, for example, by utilizing a differential display procedure, Northern analysis and/or RT-PCR.

Antibodies directed against wild type or mutant myocilin polypeptides or allelic variants thereof, which are discussed above, may also be used in disease diagnostics and prognostics. Such diagnostic methods, may be used to detect abnormalities in the level of myocilin polypeptide expression, or abnormalities in the structure and/or tissue, cellular, or subcellular location of a myocilin polypeptide. Structural differences may include, for example, differences in the size, electronegativity, or antigenicity of the mutant myocilin polypeptide relative to the normal myocilin polypeptide. Protein from the tissue or cell type to be analyzed may easily be detected or isolated using techniques which are well known to one of skill in the art, including but not limited to western blot analysis. For a detailed explanation of methods for carrying out Western blot analysis, see Sambrook et al, 1989, supra, at Chapter 18. The protein detection and isolation methods employed herein may also be such as those described in Harlow and Lane, for example, (Harlow, E. and Lane, D., 1988, "Antibodies: A Laboratory Manual", Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York), which is incorporated herein by reference in its entirety.

This can be accomplished, for example, by immunofluorescence techniques employing a fluorescently labeled antibody (see below) coupled with light microscopic, flow cytometric, or fluorimetric detection. The antibodies (or fragments thereof) useful in the present invention may, additionally, be employed histologically, as in immunofluorescence or immunoelectron microscopy, for *in situ* detection of myocilin polypeptides. *In situ* detection may be accomplished by removing a histological specimen from a patient, and applying thereto a labeled antibody of the present invention. The antibody (or fragment) is preferably applied by overlaying the labeled antibody (or fragment) onto a biological sample. Through the use of such a procedure, it is possible to determine not only the presence of the myocilin polypeptide, but also its distribution in the examined tissue. Using the present invention, one of ordinary skill will readily perceive

that any of a wide variety of histological methods (such as staining procedures) can be modified in order to achieve such *in situ* detection.

Often a solid phase support or carrier is used as a support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention. The support material may have virtually any possible structural configuration so long as the coupled molecule is capable of binding to an antigen or antibody. Thus, the support configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, test strip, etc. Preferred supports include polystyrene beads. Those skilled in the art will know many other suitable carriers for binding antibody or antigen, or will be able to ascertain the same by use of routine experimentation.

One means for labeling an anti-myocilin polypeptide specific antibody is via linkage to an enzyme and use in an enzyme immunoassay (EIA) (Voller, "The Enzyme Linked Immunosorbent Assay (ELISA)", *Diagnostic Horizons* 2:1-7, 1978, Microbiological Associates Quarterly Publication, Walkersville, MD; Voller, et al., *J. Clin. Pathol.* 31:507-520 (1978); Butler, *Meth. Enzymol.* 73:482-523 (1981); Maggio, (ed.) *Enzyme Immunoassay*, CRC Press, Boca Raton, FL, 1980; Ishikawa, et al., (eds.) *Enzyme Immunoassay*, Kigaku Shoin, Tokyo, 1981). The enzyme which is bound to the antibody will react with an appropriate substrate, preferably a chromogenic substrate, in such a manner as to produce a chemical moiety which can be detected, for example, by spectrophotometric, fluorimetric or by visual means. Enzymes which can be used to detectably label the antibody include, but are not limited to, malate dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast alcohol dehydrogenase, alpha-glycerophosphate dehydrogenase, triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase and acetylcholinesterase. The detection can be accomplished by colorimetric methods which employ a chromogenic substrate for the enzyme. Detection may also be accomplished by visual comparison of the extent of enzymatic reaction of a substrate in comparison with similarly prepared standards.

Detection may also be accomplished using any of a variety of other immunoassays. For example, by radioactively labeling the antibodies or antibody fragments, it is possible to detect fingerprint gene wild type or mutant peptides through the use of a radioimmunoassay (RIA) (see, for example, Weintraub, B., *Principles of Radioimmunoassays*, Seventh Training Course on Radioligand Assay Techniques, The Endocrine Society, March, 1986, which is incorporated by reference herein). The radioactive isotope can be detected by such means as the use of a gamma counter or a scintillation counter or by autoradiography.

It is also possible to label the antibody with a fluorescent compound. When the fluorescently labeled antibody is exposed to light of the proper wave length, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent labeling compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, α -phthalaldehyde and fluorescamine.

The antibody can also be detectably labeled using fluorescence emitting metals such as ^{152}Eu , or others of the lanthanide series. These metals can be attached to the antibody using such metal chelating groups as diethylenetriaminepentacetic acid (DTPA) or ethylenediaminetetraacetic acid (EDTA).

The antibody also can be detectably labeled by coupling it to a chemiluminescent compound. The presence of the chemiluminescent-tagged antibody is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isoluminol, theromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound may be used to label the antibody of the present invention. Bioluminescence is a type of chemiluminescence found in biological systems in, which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

Moreover, it will be understood that any of the above methods for detecting alterations in a gene or gene product or polymorphic variants can be used to monitor the course of treatment or therapy.

4.8.2. Pharmacogenomics

Knowledge of the particular alteration or alterations, resulting in defective or deficient GLC1A genes or proteins in an individual (the GLC1A genetic profile), alone or in conjunction with information on other genetic defects contributing to glaucoma (the genetic profile of glaucoma) allows a customization of the therapy for glaucoma to the individual's genetic profile, the goal of "pharmacogenomics". For example, subjects having a specific allele of a GLC1A gene may or may not exhibit symptoms of glaucoma or be predisposed to developing symptoms glaucoma. Further, if those subjects are symptomatic, they may or may not respond to a certain drug, e.g., a specific GLC1A therapeutic, but may respond to another. Thus, generation of a GLC1A genetic profile, (e.g., categorization of alterations in GLC1A genes which are associated with the development of glaucoma), from a population of subjects, who are symptomatic for glaucoma (a glaucoma genetic population profile) and comparison of an individual's GLC1A profile to the population profile, permits the selection or design of drugs that should be safer and more effective for a particular patient or patient population (i.e., a group of patients having the same genetic alteration).

For example, a GLC1A population profile can be performed, by determining the GLC1A profile, e.g., the identity of GLC1A genes, in a patient population having glaucoma. Optionally, the GLC1A population profile can further include information relating to the response of the population to a GLC1A therapeutic, using any of a variety of methods, including, monitoring: 1) the severity of symptoms associated with the GLC1A related disease, 2) GLC1A gene expression level, 3) GLC1A mRNA level, and/or 4) GLC1A protein level. and (iii) dividing or categorizing the population based on the particular genetic alteration or alterations present in its GLC1A gene or a GLC1A pathway gene. The GLC1A genetic population profile can also, optionally, indicate those particular alterations in which the patient was either responsive or non-responsive to a particular therapeutic. This information or population profile, is then useful for predicting which individuals should respond to particular drugs, based on their individual GLC1A profile.

In a preferred embodiment, the GLC1A profile is a transcriptional or expression level profile and step (i) is comprised of determining the expression level of GLC1A proteins, alone or in conjunction with the expression level of other genes, known to contribute to the same disease. The GLC1A profile can be measured in many patients at various stages of the disease.

Pharmacogenomic studies can also be performed using transgenic animals. For example, one can produce transgenic mice, e.g., as described herein, which contain a specific allelic variant of a GLC1A gene. These mice can be created, e.g., by replacing their wild-type GLC1A gene with an allele of the human GLC1A gene. The response of these mice to specific GLC1A therapeutics can then be determined.

4.8.3. Monitoring of Effects of GLC1A Therapeutics During Clinical Trials

The ability to target populations expected to show the highest clinical benefit, based on the GLC1A or disease genetic profile, can enable: 1) the repositioning of marketed drugs with disappointing market results; 2) the rescue of drug candidates whose clinical development has been discontinued as a result of safety or efficacy limitations, which are patient subgroup-specific; and 3) an accelerated and less costly development for drug candidates and more optimal drug labeling (e.g. since the use of GLC1A as a marker is useful for optimizing effective dose).

The treatment of an individual with a GLC1A therapeutic can be monitored by determining GLC1A characteristics, such as myocilin protein level or activity, GLC1A mRNA level, and/or transcriptional level. This measurements will indicate whether the treatment is effective or whether it should be adjusted or optimized. Thus, GLC1A can be used as a marker for the efficacy of a drug during clinical trials.

In a preferred embodiment, the present invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate, for example a drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a preadministration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of a myocilin protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression or activity of the myocilin protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the myocilin protein, mRNA, or genomic DNA in the preadministration sample with the myocilin protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression of a wildtype GLC1A gene or activity of a wildtype myocilin protein to higher levels than detected. Alternatively, decreased administration of

the agent may be desirable to decrease expression of a mutant GLC1A gene or activity of a mutant myocilin protein to lower levels than detected.

Cells of a subject may also be obtained before and after administration of a GLC1A therapeutic to detect the level of expression of genes other than GLC1A, to verify that the GLC1A therapeutic does not increase or decrease the expression of genes which could be deleterious. This can be done, e.g., by using the method of transcriptional profiling. Thus, mRNA from cells exposed in vivo to a GLC1A therapeutic and mRNA from the same type of cells that were not exposed to the GLC1A therapeutic could be reverse transcribed and hybridized to a chip containing DNA from numerous genes, to thereby compare the expression of genes in cells treated and not treated with a GLC1A therapeutic. If, for example a GLC1A therapeutic turns on the expression of a proto-oncogene in an individual, use of this particular GLC1A therapeutic may be undesirable.

The present invention is further illustrated by the following examples which should not be construed as limiting in any way. The contents of all cited references (including literature references, issued patents, published patent applications as cited throughout this application are hereby expressly incorporated by reference. The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See, for example, *Molecular Cloning A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989); *DNA Cloning*, Volumes I and II (D. N. Glover ed., 1985); *Oligonucleotide Synthesis* (M. J. Gait ed., 1984); Mullis et al. U.S. Patent No: 4,683,195; *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*, Vols. 154 and 155 (Wu et al. eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

The present invention is further illustrated by the following examples which should not be construed as limiting in any way. The contents of all cited references (including literature references, issued patents, published patent applications, and co-pending patent applications) cited throughout this application are hereby expressly incorporated by reference.

5.1 Genetic Linkage of Familial Open Angle Glaucoma to Chromosome 1q21-q31

Materials and Methods

Pedigree

A family in which five consecutive generations have been affected with juvenile-onset, open-angle glaucoma without iridocorneal angle abnormalities was identified. The family comprised descendants of a woman who emigrated from Germany to the midwestern United States in the late 1800s. The disease state in affected family members included onset during the first 3 decades of life, normal anterior chamber angles, high intraocular pressures, lack of systemic or other ocular abnormalities, and need for surgery to control the glaucoma in affected individuals. A total of 35 family members at 50% risk for glaucoma had complete eye examinations including visual acuity with refraction, slit-lamp biomicroscopy, applanation tomometry, gonioscopy, stereo disc photography and Humphrey, Goldmann or Octopus perimetry. Two other affected patients were ascertained by reviewing records of other ophthalmologists. Patients were considered to be affected for linkage if they had documented pressures greater than 30 mm Hg and evidence of optic nerve or visual field damage; or, if they had intraocular pressures greater than 22 mm Hg and an obviously affected child. Affected family members are characterized by an early age of diagnosis, a normal appearing trabecular meshwork, very high intraocular pressures (often above 50 mm Hg), and relatively pressure-resistant optic nerves. Figure 1 is a pictorial representation of the pedigree.

DNA typing

Blood samples were obtained from all living affected family members as well as six spouses of affected patients with children. 10ml blood were obtained from each patient in EDTA-containing glass tubes. DNA was prepared from the blood using a non-organic extraction procedure (Grimberg, J. et al. Nucl. Acids Res 17, 8390 (1989)). Short tandem repeat polymorphisms (STRPs) distributed across the entire autosomal genome were selected from the literature or from those kindly provided by J.L. Weber. The majority were [dC-dA]-[dG-dT] dinucleotide repeats. Oligonucleotide primers flanking each STRP were synthesized using standard phosphoramidite chemistry (Applied Biosystems model 391 DNA synthesizer). Amplification of each STRP was performed with 50 ng. of each patient's DNA in a 8.35 l PCR containing each of the following: 1.25 l 10 X buffer (100mM Tris-HCl pH 8.8, 500 mM KCl, 15 mM MgCl₂, 0.01% w/v gelatin), 300 M each of dCTP, dGTP and dTTP, 37M dATP, 50pmoles each primer, 0.25 l ³⁵S-dATP (Amersham, >1000 Ci mmol⁻¹), and 0.25 U *Taq* polymerase (Perkin-Elmer/Cetus). Samples were incubated in a DNA thermocycler (Perkin-Elmer/Cetus) for 35 cycles under the following conditions: 94C for 30 s, 55C for 30 s, and 72C for 30 s. Following amplification, 5l of stop solution (95% formamide, 10mM NaOH, 0.05% Bromophenol Blue, 0.05% Xylene Cyanol) was added to each sample. Following denaturation for 3 min at 95C, 5 l of each sample was immediately loaded onto prewarmed polyacrylamide gels (6% polyacrylamide, 7 M urea) and electrophoresed for 3-4h. Gels were then placed on Whatman, 3mm paper and dried in a slab gel dryer. Autoradiographs were created by exposing Kodak Xomat AR film to the dried gels for 24-36h.

Linkage analysis

Genotypic data from the autoradiographs were entered into a Macintosh computer. A Hypercard-based program (Nichols, BE et al., Am J Hum Genet 51 A369 (1992)) was used to store and retrieve marker data as well as to export it to a DOS-compatible machine for analysis with the computer program LINKAGE (version 5.1) (Lathrop, GM and LaLouel, JM 359, 794-801 (1992)). Allele frequencies were assumed to be equal for each marker. The MLINK routine was used for pairwise analysis. The relative odds of all possible orders of the disease and two markers (D1S191 and D1S194) was performed under the ILINK program. Significance of linkage was evaluated using the standard criterion ($Z_{\max} > 3.0$).

Results

clinical findings

5 All of the 37 family members studied were at 50% risk of having the disease because of a known affected parent or sibling. Nineteen of these patients had elevated intraocular pressures and visual field defects consistent with the diagnosis of primary open angle glaucoma. Three more patients had moderately elevated intraocular pressures and obviously affected children.

linkage analysis

10 Over 90 short tandem repeat polymorphisms were typed the family before linkage was detected with markers that map to the long arm of chromosome 1. Two-point maximum likelihood calculations using all available family members and 33 chromosome 1 markers revealed significant linkage to eight of them (Table 2). D1S212 was fully informative for all affected members of the family, and pairwise linkage
15 analysis produced a lod score of 6.5 ($= 0$). Multipoint linkage analysis did not add to the peak lod score. The glaucoma locus was therefore determined to be located in a region of about 20 centiMorgans (cM) in size between D1S191 and D1S194. Both of these markers demonstrated multiple recombinants (two and three, respectively) in affected individuals in the family. The order D1S191-glaucoma-D1S194 was more than
20 1,000 times more likely than the other two possible orders.

Table 6 Pairwise linkage data

		Recombination Fraction					Z_{ma}	Locu		$\hat{\theta}$	
		0.15	0.20	0.25	0.30	0.40					
							x	s			
25	D1S212	6.0	5.4	4.8	4.2	3.6	2.9	1.4	6.5	0.00	1
	D1S215	5.1	4.6	4.0	3.5	2.9	2.3	1.0	5.6	0.00	1
	D1S218	4.7	4.3	3.8	3.3	2.7	2.2	1.0	5.2	0.00	1
	D1S238	4.4	4.2	3.9	3.4	2.9	2.4	1.2	4.4	0.04	1
	D1S117	3.8	3.6	3.3	2.8	2.3	1.8	0.7	3.8	0.04	1q
30	D1S104	3.2	2.9	2.6	2.3	2.0	1.6	0.7	3.4	0.00	1q21-q23
	D1S191	3.0	3.2	3.0	2.7	2.4	1.9	0.9	3.2	0.09	1
	D1S196	2.9	2.6	2.3	2.0	1.6	1.3	0.5	3.1	0.00	1

Table 6 Pairwise linkage data

Recombination fraction

0.05 0.19

5 5.2 Genetic Fine Mapping of the Juvenile Primary Open Angle
Glaucoma Locus and Identification and Characterization of a Glaucoma
Gene

10 Once primary linkage has been identified, the next step in identifying any
disease gene by positional cloning is the narrowing of the candidate locus to the smallest
possible genetic region. The initial study described in Example 5.1 demonstrated that a
primary open angle glaucoma gene lies within an approximately 20 cM region flanked
by markers D1S194 and D1S191 on chromosome 1q. Additional markers and families
were obtained and used to refine the genetic locus to a 2.5 cM region using two of these
families. The third family should allow the interval to be further narrowed.

15 In addition to the family resources, polymorphic DNA markers and
genetic maps were used to refine the 1q glaucoma locus. Using STRPs, the genotype of
each family member was determined. Amplification of each STRP was performed using
the following protocol:

20 1) Dilute genomic DNA (about 1g/l) 1/50 i.e. 20l "stock" DNA and
980 dd H₂O.

2) Use 2.5l of "dilute" DNA as template for PCR

3) Prepare PCR reaction mix as follows:

25 1.25l 10 X Buffer (Stratagene)
0.12l of each primer (50pmoles each primer)
0.5l dNTPs (5mM C,T,&G and 0.625 mM A "cold")
3.5l dd H₂O
0.25l ³⁵S-dATP
30 0.1l Taq polymerase
oil (one drop)

4) Perform PCR at optimal conditions for given primers (usually 94 30 s,
55 30s and 72 30 s) and run for 35 cycles.

5) Add 5l stop solution (95% formamide, 10mM NaOH, 0.05% bromophenol blue, 0.05% xylene cyanol) to each tube.

5 6) Denature samples at 95C for 3 minutes and load immediately onto a prewarmed polyacrylamide gel.

7) Dry gels on Whatmann paper and expose autoradiography film for 1-2 days.

10

Where possible, multiple loadings of different STRPs on gels were performed. Up to 6 markers per gel have been successfully loaded. In addition, the PCR amplification (up to three markers) have been successfully multiplexed. The juvenile glaucoma gene is believed to lie between markers AFM238 and AT3 (an 8 centimorgan interval) based on observed recombinations within the families studied. Haplotypic analysis between families has further narrowed this interval to the 2 centimorgan interval between D1S210 and AT3.

Since the genetic interval has been narrowed significantly physical mapping strategies can be used. The closest flanking markers to screen total human genomic yeast artificial chromosome (YAC) libraries to identify YACs mapping to the region of interest. The CEPH and CEPH mega-YAC libraries can be used for this purpose (available from the Centre d'Etude du Polymorphisme Humain (CEPH) Paris, France). Forty-four percent of the clones in the CEPH mega-YAC library have an average size of 560 kb, an additional 21% have an average size of 800 kb, and 35% have an average size of 120 kb. This library is available in a gridded micro-titer plate format such that only 50-200 PCR reactions need to be performed using a specific sequence tagged site (STS) to identify a unique YAC containing the STS. The YAC contigs identified by CEPH have been used to begin constructing a contig across the 1q candidate region (see Figure 3). YAC contigs using YAC ends can be constructed to identify additional YACs. YAC ends can be rescued using anchored PCR (Riley, J. et al (1990) *Nucleic Acids Res* 18:2887-2890), the ends can then be sequenced and the sequence can be used to develop a sequence tagged site (STS). The STS can be used to rescreen the YAC library to obtain an overlapping adjacent YAC.

Because some YACs have been shown to be chimeric or to contain deletions or rearrangements, particularly those from the mega YAC library, the correctness of each YAC contig should be verified by constructing a pulse field map of the region. In addition, chimeric YACs are minimized by ensuring that the YAC maps to a single chromosome by fluorescent in situ hybridization (FISH) or that the two YAC ends map to the same chromosome using monochromosomal somatic cell hybrids (NIGMs Panel 2). In addition, the YAC chimera problem can be minimized by not relying on any single YAC to span a given chromosome segment, but rather by obtaining at least two overlapping independent YACs to ensure coverage of a given region.

Once a YAC contig spanning the candidate region has been isolated, this reagent can be used to generate additional genetic markers for potentially finer genetic mapping. In addition, the YACs can be used to make higher resolution physical mapping reagents such as region specific lambda and cosmid clones. Lambda and cosmid clones can be used for isolation of candidate genes. A modification of "exon trapping" (Duyk, G.M. (1990) *Proc Natl Acad Sci USA* 87:8995-8999) known as exon amplification (Buckler, A.J. (1991) *Proc Natl Acad Sci USA* 88:4005-4009) can be used to identify exons from genes within the region. Exons trapped from the candidate region can be used as probes to screen eye cDNA libraries to isolate cDNAs. Where necessary, other strategies can be utilized to identify genes in genomic DNA including screening cDNA libraries with YAC fragments subcloned into cosmids, zoo blot analysis, coincidence cloning strategies such as direct selection of cDNAs with biotin-streptavidin tagged cosmid clones (Morgan, J.G. et al (1992) *Nucleic Acid Res* 20 (19):5173-5179), and HTF island analysis (Bird, A.P. (1987) *Trends Genet* 3:342-247). Promising genes will be further evaluated by searching for mutations using GC-clamped denaturing gradient gel electrophoresis (Sheffield, V.C. et al (1989) *Genomics* 16:325-332), single strand conformational gel polymorphism (SSCP) analysis (Orita, M. et al (1989) *Proc Natl Acad Sci USA* 86:2766-2770) and direct DNA sequencing.

5.3 Primer Pairs for Use In Identifying Subjects Having a Predisposition to Glaucoma

Two primer pairs that can be used in conjunction with the polymerase chain reaction to amplify a 190 base pair sequence from human genomic DNA that harbors mutations causing glaucoma (primers 1 and 2 in Table 7) have been identified.

TABLE 7

Primer 1	forward - ATACTGCCTAGGCCACTGGA (SEQ ID NO. 12) reverse - CAATGTCCGTGTAGCCACC (SEQ ID NO. 13)
Primer 2	forward - GAACTCGAACAAACCTGGGA (SEQ ID NO. 14) reverse - CATGCTGCTGTACTTATAGCGG (SEQ ID NO. 15)

These primers were used to screen 410 patients with glaucoma and 81 normal individuals. Four amino acid altering sequence changes were detected in a total of 12 glaucoma patients (2.9%). No amino acid altering sequence changes were observed in the normal individuals.

The prevalence of mutations in the segment of DNA amplified by these primer pairs suggest that use of these primers in conjunction with an appropriate detection method can be used to identify a predisposition to glaucoma in approximately 100 thousand patients in the United States alone.

5.4 Additional Primer Pairs and Their Use In Identifying Subjects Having a Predisposition to Glaucoma

The study was approved by the Human Subjects Review Committee at the University of Iowa and informed consent was obtained from all study participants. Primary open angle glaucoma was defined as the presence of an intraocular pressure over 21 mm Hg as well as evidence of glaucomatous optic nerve head damage. Visible optic nerve head damage alone was accepted if there was documented enlargement of the optic nerve head cup. Otherwise, both a large optic nerve head cup with a thin neural rim and characteristic optic nerve related visual field loss were required. Patients were excluded if they had a history of eye surgery prior to the diagnosis of glaucoma or evidence of secondary glaucoma, such as exfoliation or pigment dispersion. Normal volunteers were over 40 years of age, had intraocular pressures under 20 mm Hg, and had no family or personal history of glaucoma. 716 unrelated patients affected with primary open angle glaucoma (POAG) and 91 volunteers were screened for mutations in the coding sequence of the GLC1A gene. This was accomplished with an electrophoretic procedure known as single strand conformation polymorphism analysis

(SSCP). The sequences of the oligonucleotide primers used for the GLC1A assay are presented in Table 8.

Table 8

5	Primer Pairs		
	Exon	Forward Primer	Reverse Primer
10	1	SEQ ID No. 16	SEQ ID No. 17
	1	SEQ ID No. 18	SEQ ID No. 19
	1	SEQ ID No. 20	SEQ ID No. 21
	1	SEQ ID No. 22	SEQ ID No. 23
	1	SEQ ID No. 24	SEQ ID No. 25
	1	SEQ ID No. 26	SEQ ID No. 27
15	2	SEQ ID No. 28	SEQ ID No. 29
	3	SEQ ID No. 30	SEQ ID No. 31
	3	SEQ ID No. 32	SEQ ID No. 33
	3	SEQ ID No. 34	SEQ ID No. 35
	3	SEQ ID No. 36	SEQ ID No. 37
20	3	SEQ ID No. 38	SEQ ID No. 39
	3	SEQ ID No. 40	SEQ ID No. 41

Mutations were confirmed with automated DNA sequencing. 227 of the patients (32%) were ascertained because of a positive family history of glaucoma while 402 (56%) were ascertained consecutively in a single glaucoma clinic (the University of Iowa). Overall, 563 of the patients were ascertained in Iowa, 97 in Australia and the remainder from elsewhere in the United States. All of the normal volunteers were collected in Iowa. More than 75% of the patients in each group were Caucasian. A portion of the GLC1A gene had been previously evaluated for mutations in 330 of these same glaucoma patients and all 91 normal volunteers (see above). However, in this study, the entire coding region was evaluated. An additional 505 unrelated control individuals with an unknown glaucoma status were also evaluated for sequence changes. Three hundred and eighty of these control patients had been previously screened for mutations in a portion of exon 3. 184 of these general population controls were connected in Iowa and 13 in Australia. Family members of the probands found to

harbor GLC1A sequence changes were also evaluated for mutations. Efforts were made to examine or review the medical records of all molecularly affected family members. The age of onset and the highest recorded intraocular pressures were associated with six different mutations were evaluated with a Kruskal-Wallis non-parametric analysis of variance. All p values were two-tailed. In the four largest families, co-segregation of a GLC1A mutation and the disease phenotype was evaluated with the LOD score method as described above

5.5 Cloning and Sequencing Human and Mouse GLC1A and Northern Blot Analysis of Expression

BAC screening. BAC clones containing the human GLC1A gene were identified by screening human BAC library pools (Research Genetics, Huntsville, AL) with a PCR-based assay. One microliter of BAC pool DNA was used as template in an 8.35 μ l PCR reaction containing 1.25 μ l of 10X buffer (100 mM tris-HCl, pH 8.3, 500 mM KCl, 15 mM MgCl₂); deoxynucleotides dCTP, dATP, dTTP, and dGTP (300 μ M each); 1 pmol of each primer; and 0.25 units of *Taq* polymerase (Boehringer Mannheim, Indianapolis, IN). The primers used in the screening assay were specific for exon three of GLC1A (FWD: 5' ATACTGCCTAGGCCACTGGA 3' (SEQ ID No. 34) and REV: 5' CAATGTCCGTGTAGCCACC 3' (SEQ ID No. 35)). Samples were denatured at 94° C for 5 minutes and incubated for 35 cycles at 94° C 30s, 55° C 30s, 72° C 30s in a DNA thermocycler (Omnigene, Teddington, Middlesex, UK). After amplification, 5 μ l of stop solution (95% formamide, 10 mM NaOH, 0.5% bromophenyl blue, 0.05% xylene cyanol) were added. Amplification products were electrophoresed on 6% polyacrylamide-5% glycerol gels at 50 W for approximately 2 hours. After electrophoresis, gels were stained with silver nitrate (Bassam 1991). A BAC containing the mouse GLC1A orthologue was identified by screening the mouse 129 BAC library pools (Research Genetics, Huntsville AL). Primers specific for exon three of the human GLC1A gene (FWD: 5' TGGCTACCACGGACAGTTC 3' (SEQ ID No. 36) and REV: 5' CATTGGCCACTGACTGCTTA 3' (SEQ ID No. 37) were used for a primary PCR-based screen as described above. The primary screen identified sub-pools of BACs which contained the mouse GLC1A gene. Filters blotted with the BACs in the subpools (Research Genetics, Huntsville, AL) were screened by hybridization with a digoxigenin probe using the Genius System hybridization kit (Boehringer Mannheim, Indianapolis, IN). Digoxigenin labeled probe for hybridization was generated by PCR amplifying 50

ng of mouse 129 DNA in a 25 μ l reaction containing 3.75 μ l of 10X buffer; 1.5 μ l of labeling dNTP mixture (1 mM dATP, 1 mM dCTP, 1mM dGTP 0.65 mM dTTP, and 0.35 mM of digoxigenin conjugated dUTP); 7.6 pmoles each of FWD and REV primer; and 1.25 units of Taq polymerase (Boehringer Mannheim, Indianapolis, IN). PCR reaction conditions were as described above. Hybridization conditions were as recommended by the manufacturer.

The human GLCIA cDNA sequence was used to select PCR primers that produced an amplification product of identical size when using both human and mouse genomic DNA as template. The amplification products were sequenced to confirm that they were from the human GLCIA gene and the mouse orthologue of this gene. The PCR primers were then used to screen both a human and mouse BAC library. Both human and mouse BACs containing the GLCIA gene were identified, subcloned into plasmids, and several clones covering each GLCIA gene were identified. These subclones were used to generate both human and mouse genomic GLCIA sequence.

Subcloning. The mouse and human BACs containing the GLCIA gene were digested with either EcoR1, Aval, Acc1, or BamH1 and ligated into either pT7-blue (Novagen, Milwaukee, WI) or pUC19.

Sequencing. PCR products and BAC subclones were sequenced with fluorescent dideoxynucleotides on an Applied Biosystems (ABI) model 373 or 377 automated sequencer.

GLCIA CA repeat polymorphisms. The CA repeat polymorphism upstream of the GLCIA gene was PCR amplified with primers 5'-TTCCTTCAGGTTGGGAGATG-3' (SEQ ID No. 42) and 5'-GAGAGCACCAGGAGATGGAG-3' (SEQ ID No. 43). The PCR reaction conditions were as described in the BAC screening section. Allele frequencies for the upstream polymorphism are: Allele 1, 1.1%; Allele 2, 2.2%; Allele 3, 48.9%; Allele 4, 1.1%; Allele 5, 21.1%; Allele 6, 25.6%. Allele frequencies for the downstream polymorphism are: Allele 1, 25.3%; Allele 2, 13%, Allele 3, 60.3%, Allele 4, 1.4%.

Sequence comparison. DNA sequences were aligned and contigs were formed using the Sequencher DNA analysis package (DNA Codes, Ann Arbor, MI). Putative enhancer and promoter elements were identified using the internet resource TESS (<http://agave.humgen.upenn.edu/utess/>) and the transcription factor binding site data set TRANSFAC v3.2. The predicted protein sequence was analyzed with PROSITE, Tmpred, NetOgly, and SignalP software packages available on the internet at

<http://expasy.hcuge.chsprot/prosite.html>;

http://ulrec3.unil.ch/software/TMPED_form.html;

<http://genome.cbs.dtu.dk/services/netOGLYC/>;

<http://www.cbs.dtu.dk/services/SignalP/>. Data base searches for expression of the

- 5 GLCIA gene used the program BLAST and the data bases dbest and NR available on the internet at <http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-blast?Jform=0>.

Northern blot analysis. Human Multiple Tissue Northern (MTN) blots (Clontech, San Francisco, CA) were probed either with the entire human GLCIA cDNA sequence or with a section of exon three of the human GLCIA gene corresponding to
10 codon 315 to the termination site. The probes were labeled with ³²P-(dCTP) using Ready-To-Go DNA Labeling Beads (-dCTP) (Pharmacia Biotech, Piscataway, NJ). Hybridization was for 16 hours at 42°C in 50% formamide, 5X standard saline citrate (5X SSC: 0.75M sodium chloride, 0.075M sodium acetate), 1X Denhardt's solution, 20mM phosphate buffer (pH 7.5), 1% sodium dodecyl sulfate (SDS), 100 µg/ml salmon
15 sperm DNA, and 10% dextran sulfate. Following hybridization, blots were washed twice at room temperature in 1X SSC, rinsed twice in 1X SSC / 1% SDS at 65°C, and washed once in 0.1X SSC, 0.1% SDS to confirm the specificity of the hybridization. Autoradiography was performed with Kodak XAR-5 film at -70°C with DuPont Cronex Lightning Plus intensifying screens (DuPont, Wilmington, DE).

20

Claims

1. An isolated nucleic acid molecule comprising a nucleic acid molecule or the
5 complement of a nucleic acid molecule set forth in any of SEQ ID Nos. 16, 17, 18, 19,
20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42 or
43.
2. An isolated nucleic acid molecule comprising a nucleic acid molecule or the
10 complement of a nucleic acid molecule obtained by amplifying a GLC1A gene with a
primer pair selected from the group consisting of SEQ ID Nos 16 and 17, SEQ ID Nos
18 and 19, SEQ ID Nos 20 and 21, SEQ ID Nos 22 and 23, SEQ ID Nos 24 and 25, SEQ
ID Nos 26 and 27, SEQ ID Nos 28 and 29, SEQ ID Nos 30 and 31, SEQ ID Nos 32 and
33, SEQ ID Nos 34 and 35, SEQ ID Nos 36 and 37, SEQ ID Nos 38 and 39, SEQ ID
15 Nos 40 and 41, SEQ ID Nos 42 and 43.
3. An isolated nucleic acid molecule of claim 2, which appears within Exon 1 of Figure
1 or is the complement of a a nucleic acid molecule, which appears within Exon 1.
- 20 4. An isolated nucleic acid molecule of claim 2, which appears within Exon 2 of Figure
1 or is the complement of a a nucleic acid molecule, which appears within Exon 2.
5. An isolated nucleic acid molecule of claim 2, which appears within Exon 3 of Figure
1 or is the complement of a a nucleic acid molecule, which appears within Exon 3.
25
6. An isolated nucleic acid of claim 3, wherein the primer pair is comprised of a
member selected from the group consisting of: SEQ ID Nos. 16 and 17; SEQ ID Nos. 18
and 19; SEQ ID Nos. 20 and 21; SEQ ID Nos. 22 and 23; SEQ ID Nos. 24 and 25; and
SEQ ID Nos. 26 and 27..
30
7. An isolated nucleic acid of claim 4, wherein the primer pair is comprised of SEQ ID
Nos. 28 and 29.

8. An isolated nucleic acid of claim 5, wherein the primer pair is comprised of SEQ ID Nos 30 and 31, SEQ ID Nos 32 and 33, SEQ ID Nos 34 and 35, SEQ ID Nos 36 and 37, SEQ ID Nos 38 and 39, SEQ ID Nos 40 and 41.

5 9. An isolated nucleic acid of claim 2, which is upstream of the GLC1A gene and is amplified by SEQ ID Nos 42 and 43.

10. A method for determining whether a subject has or has the potential for developing primary open angle glaucoma, comprising the steps of:

- 10 a) obtaining a biological sample containing genomic DNA or a complement thereof from a subject;
- b) performing an amplification on the genomic DNA using a primer pair selected from the group consisting of SEQ ID Nos 16 and 17, SEQ ID Nos 18 and 19, SEQ ID Nos 20 and 21, SEQ ID Nos 22 and 23, SEQ ID Nos 24 and 25, SEQ ID Nos 26 and 27, SEQ ID Nos 28 and 29, SEQ ID Nos 30 and 31, SEQ ID Nos 32 and 33, SEQ ID Nos 34 and 35, SEQ ID Nos 36 and 37, SEQ ID Nos 38 and 39, SEQ ID Nos 40 and 41, SEQ ID Nos 42 and 43, thereby obtaining an amplification product; and
- 15 c) analyzing the amplification product for the presence of a mutation, wherein the presence of a mutation indicates that the subject has or has the potential for developing primary open angle glaucoma.
- 20
- the
- potential for developing primary open angle glaucoma.

25 11. A screening method of claim 10, wherein in step c), the amplification product is analyzed using single strand conformation polymorphism (SSCP) analysis.

12. A screening method of claim 10, wherein in step c), the amplification product is analyzed by sequencing.

30

13. A kit for diagnosing a subject as having primary open angle glaucoma comprising:

a) a primer pair selected from the group consisting of: SEQ ID Nos 16 and 17, SEQ ID Nos 18 and 19, SEQ ID Nos 20 and 21, SEQ ID Nos 22 and 23, SEQ ID Nos 24 and 25, SEQ ID Nos 26 and 27, SEQ ID Nos 28 and 29, SEQ ID Nos 30 and 31, SEQ ID Nos 32 and 33, SEQ ID Nos 34 and 35, SEQ ID Nos 36 and 37, SEQ ID Nos 38 and 39, SEQ ID Nos 40 and 41, SEQ ID Nos 42 and 43.; and

b) instructions for using the primer pair to perform an amplification.

[illegible]

[illegible]

[illegible]

Figure 1C. Exon 3

[illegible]

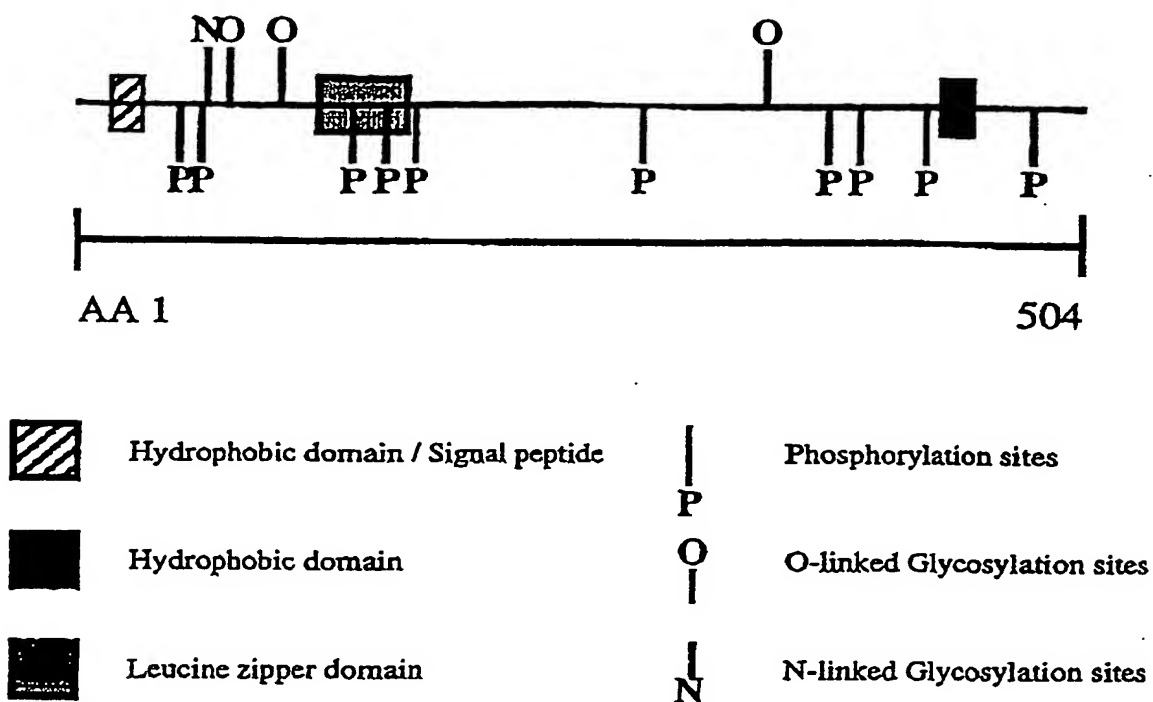


Figure 2

Figure 3 Sequence conservation between huGLC1A and moGLC1A

1	huGLC1A	MRFFCARCCS	FGPEMPAVQL	LLLACLVWIDV	GARTAQLRKA	NDQSGROQYT	H
	moGLC1A	
		MPALHL	LFLACLVWGM	GARTAQFRKA	NDRSGROQYT		
51	huGLC1A	FSVASPNSS	CPEQSQAMSV	IHNLRDSST	QRDLLEATKA	RLSSLESLLH	C
	moGLC1A	FTVASPNSS	CPREDQMSA	IQDLQDSSI	QHADLESTKA	RVRSLLESLLH	
101	huGLC1A	QLTLDQAARP	QETQEGLORE	LGTLRERDQ	LETQTRLET	AYSNLLRDKS	
	moGLC1A	QMTLGRVIGT	QEAQEGLOQ	LGALRRERDQ	LETQTRDLEA	AYNNLLRDKS	
151	huGLC1A	VLEEEKRLR	QENENLARRL	ESSSQEVARL	RRGQCPQTRD	TARAVPPGSR	
	moGLC1A	ALEEEKRQLE	QENEDLARRL	ESSSEEVTRL	RRGQCPSTQY	PSQDMLPGSR	
201	huGLC1A	EVSWNLDTL	AFQELKSELT	EVPASRIKE	SPSGYLRSGE	GDTGGELWW	
	moGLC1A	EVSQWNLDTL	AFQELKSELT	EVPASQILKE	NPSGRPRSKS	GDKGCGALWW	
251	huGLC1A	VGEPLTLRTA	ETITGKYGVW	MRDPKPTYPY	TQETTWRIIDT	VGTDVRQVFE	R K
	moGLC1A	VGEFVTLRTA	ETTLGKYGVW	MRDPKPIHPY	TQESTWRIDT	VGTEIRQVFE	
301	huGLC1A	YDLISQFMQ	YPSKVHILPR	PLESTGAVVY	SGSLYFQGA	SRTVIRYELN	
	moGLC1A	YSQISQFEQ	YPSKVHVLPR	ALESTGAVVY	AGSLYFQGA	SRTVVRVELD	
351	huGLC1A	TETVKAKEI	PGAGYHGQFP	YSWGGYTDID	LAVDEAGLWV	IYSTDEAKGA	S V 1 M G 2
	moGLC1A	TETVKAKEI	PGAGYHGHP	YAWGGYTDID	LAVDEAGLWV	IYSTEAKGA	
401	huGLC1A	IVLSKLNPN	LELEQIWEIN	IRKQSVANAF	IIQGTLYTVS	SYTSADATVN	H H V
	moGLC1A	IVLSKLNPN	LELERIWEIN	IRKQSVANAF	VIOGILYTVS	SYSSAHATVN	
451	huGLC1A	FAYDTGTGIS	KILTIPFKNR	YKYSSMIDYN	PLEKKLEAWD	NLNMVTYDIK	C N R
	moGLC1A	FAYDTGTGTS	KILTIPFTNR	YKYSSMIDYN	PLERKLEAWD	NENMVTYDIK	
501	huGLC1A	LSRM					
	moGLC1A	LIEM					

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Stone, Edwin M.
Sheffield, Val C.
Alward, Wallace L.M.
Fingert, John

(ii) TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS

(iii) NUMBER OF SEQUENCES: 43

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
(B) STREET: One Post Office Square
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109-2170

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Unassigned
(B) FILING DATE: Concurrently Herewith

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Arnold, Beth E.
(B) REGISTRATION NUMBER: 35,430
(C) REFERENCE/DOCKET NUMBER: UIA-010.28

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617-832-1000
(B) TELEFAX: 617-832-7000

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2800 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	AGCGCAGGGG AGGAGAAGAA AAGAGAGGGA TAGTGTATGA GCAAGAAAGA CAGATTCATT	60
5	CAAGGGCAGT GGAATTGAC CACAGGGATT ATAGTCCACG TGATCCTGGG TTCTAGGAGG	120
	CAGGGCTATA TTGTGGGGGG AAAAAATCAG TTCAAGGGAA GTCGGGAGAC CTGATTTCTA	180
10	ATACTATATT TTTCTTTTAC AAGCTGAGTA ATTCTGAGCA AGTCACAAGG TAGTAACTGA	240
	GGCTGTAAGA TTAAGTAGTT TCTCCTTATT AGGAACTCTT TTTCTCTGTG GAGTTAGCAG	300
	CACAAGGGCA ATCCCGTTTC TTTTAACAGG AAGAAAACAT TCCTAAGAGT AAAGCCAAAC	360
15	AGATTCAAGC CTAGGTCTTG CTGACTATAT GATTGGTTTT TTGAAAAATC ATTTTCAGCGA	420
	TGTTTACTAT CTGATTCAGA AAATGAGACT AGTACCCTTT GGTCAGCTGT AAACAAACAC	480
20	CCATTTGTAA ATGTCTCAAG TTCAGGCTTA ACTGCAGAAC CAATCAAATA AGAATAGAAT	540
	CTTTAGAGCA AACTGTGTTT CTCCACTCTG GAGGTGAGTC TGCCAGGGCA GTTTGGAAAT	600
	ATTTACTTCA CAAGTATTGA CACTGTTGTT GGTATTAACA ACATAAAGTT GCTCAAAGGC	660
25	AATCATTATT TCAAGTGGCT TAAAGTTACT TCTGACAGTT TTGGTATATT TATTGGCTAT	720
	TGCCATTTGC TTTTGTGTTT TTCTCTTTGG GTTTATTAAT GTAAAGCAGG GATTATTAAC	780
30	CTACAGTCCA GAAAGCCTGT GAATTTGAAT GAGGAAAAAA TTACATTTTT GTTTTTACCA	840
	CCTTCTAACT AAATTTAACA TTTTATTCCA TTGCGAATAG AGCCATAAAC TCAAAGTGGT	900
	AATAACAGTA CCTGTGATTT TGTCAATACC AATAGAAATC ACAGACATTT TATACTATAT	960
35	TACAGTTGTT GCAGATACGT TGTAAGTGAA ATATTTATAC TCAAAACTAC TTTGAAATTA	1020
	GACCTCCTGC TGGATCTTGT TTTTAACATA TTAATAAAAC ATGTTTAAAA TTTTGATATT	1080
40	TTGATAATCA TATTTTATTA TCATTTGTTT CCTTTGTAAT CTATATTTTA TATATTTGAA	1140
	AACATCTTTC TGAGAAGAGT TCCCCAGATT TCACCAATGA GGTCTTGGC ATGCACACAC	1200
	ACAGAGTAAG AACTGATTTA GAGGCTAACA TTGACATTGG TGCCTGAGAT GCAAGACTGA	1260
45	AATTAGAAAG TTCTCCCAA GATACACAGT TGTTTTAAAG CTAGGGGTGA GGGGGGAAAT	1320
	CTGCCGCTTC TATAGGAATG CTCTCCCTGG AGCCTGGTAG GGTGCTGTCC TTGTGTTCTG	1380
50	GCTGGCTGTT ATTTTTCTCT GTCCCTGCTA CGTCTTAAAG GACTTGTTG GATCTCCAGT	1440
	TCCTAGCATA GTGCCTGGCA CAGTGCAGGT TCTCAATGAG TTTGCAGAGT GAATGGAAAT	1500
	ATAAACTAGA AATATATCCT TGTTGAAATC AGCACACCAG TAGTCCTGGT GTAAGTGTGT	1560
55	GTACGTGTGT GTGTGTGTGT GTGTGTGTGT GTAAAACCAG GTGGAGATAT AGGAACTATT	1620

ATTGGGGTAT GGGTGCATAA ATTGGGATGT TCTTTTAA AAGAACTCC AAACAGACTT 1680
CTGGAAGGTT ATTTTCTAAG AATCTTGCTG GCAGCGTGAA GGCAACCCCC CTGTGCACAG 1740
5 CCCCACCCAG CCTCACGTGG CCACCTCTGT CTTCCCCCAT GAAGGGCTGG CTCCCCAGTA 1800
TATATAAACC TCTCTGGAGC TCGGGCATGA GCCAGCAAGG CCACCCATCC AGGCACCTCT 1860
10 CAGCACAGCA GAGCTTTTCCA GAGGAAGCCT CACCAAGCCT CTGCAATGAG GTTCTTCTGT 1920
GCACGTTGCT GCAGCTTTGG GCCTGAGATG CCAGCTGTCC AGCTGCTGCT TCTGGCCTGC 1980
CTGGTGTGGG ATGTGGGGGC CAGGACAGCT CAGCTCAGGA AGGCCAATGA CCAGAGTGGC 2040
15 CGATGCCAGT ATACCTTCAG TGTGGCCAGT CCCAATGAAT CCAGCTGCCC AGAGCAGAGC 2100
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20 GAGGCCACCA AAGCTCGACT CAGCTCCCTG GAGAGCCTCC TCCACCAATT GACCTTGGAC 2220
CAGGCTGCCA GGCCCCAGGA GACCCAGGAG GGGCTGCAGA GGGAGCTGGG CACCCTGAGG 2280
CGGGAGCGGG ACCAGCTGGA AACCCTAAACC AGAGAGTTGG AGACTGCCTA CAGCAACCTC 2340
25 CTCCGAGACA AGTCAGTTCT GGAGGAAGAG AAGAAGCGAC TAAGGCAAGA AAATGAGAAT 2400
CTGGCCAGGA GGTGGAAAG CAGCAGCCAG GAGGTAGCAA GGCTGAGAAG GGGCCAGTGT 2460
30 CCCCAGACCC GAGACACTGC TCGGGCTGTG CCACCAGGCT CCAGAGAAGG TAAGAATGCA 2520
GAGTGGGGGG ACTCTGAGTT CAGCAGGTGA TATGGCTCGT AGTGACCTGC TACAGGCGCT 2580
CCAGGCCTCC CTGCCTGCCC TTTCTCCTAG AGACTGCACA GCTAGCACA GACAGATGAA 2640
35 TTAAGGAAAG CACAGCGATC ACCTTCAAGT ATTACTAGTA ATTTAGCTCC TGAGAGCTTC 2700
ATTTAGATTA GTGGTTCAGA GTTCTTGTGC CCCTCCATGT CAGTTTTCAC AGTCCATAGC 2760
40 AAAAGGAGAA ATAAAAGGAC CGGGTGAGAT GTGTCTGCAT 2800

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 680 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: DNA (genomic)

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACCATGTTG GCCAGGCTGG TCTCGAACTC CTGACCTCAG GTGATCCGCC TGCCTCGGCC 60

TCCCAAAGTG CTGGGATTAC AGGCATGAGC CACCACGCCT GGCCGGCAGC CTATTTAAAT 120
 GTCATCCTCA ACATAGTCAA TCCTTGGGCC ATTTTTTCTT ACAGTAAAAT TTTGTCTCTT 180
 5 TCTTTTAATG CAGTTTCTAC GTGGAATTTG GACACTTTGG CCTTCCAGGA ACTGAAGTCC 240
 GAGCTAACTG AAGTTCCTGC TTCCCGAATT TTGAAGGAGA GCCCATCTGG CTATCTCAGG 300
 AGTGGAGAGG GAGACACCGG TATGAAGTTA AGTTTCTTCC CTTTTGTGCC CACATGGTCT 360
 10 TTATTCATGT CTAGTGCTGT GTTCAGAGAA TCAGTATAGG GTAAATGCCC ACCCAAGGGG 420
 GAAATTAAC TCCCTGGGAG CAGAGGGAGG GGAGGAGAAG AGGAACAGAA CTCTCTCTCT 480
 15 CTCTCTGTTC CTTTGTGAGA GCAGGTCTGC AGGAGTCAGC CTTTCCCTAA CAAAGCCCTC 540
 TATCCTATCA CCCACACTTG GGAGGCTGGG CTGGGCTGCA CAGGGCAAGA TGAGAGATGT 600
 GTTGATTTC TCCACTTGAT TGTCATGTAG AATTAGATAT ACTTGAGAAG TTACATTTTT 660
 20 CAGTAGCGCC TTCATATCTT 680

(2) INFORMATION FOR SEQ ID NO:3:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2000 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTACAACTG ATACTGAGTG AATTGTACTT TAAATATTTT ATAGCTCCCA CTCCCATGCA 60
 40 TGCCCCCTCAG TGATAGCAAT AATTGTCAAT AACATGAAAC ACAGATTGAT CATATAGCAT 120
 TTACCATATA TTTACTCTAT ACCAAGCACT TAACATATAT AATTACATTT AAAATTTACA 180
 ACAGCCCTAC TACCCAAAAC ACTATTAGTA TCCCCTTTTA CACATGCGAT AACTGAGGCG 240
 45 TAGAGAGCTA AGTAACTTAC TGAAAGTCAC ACAGCCAGCG GGTGGTAGAG CCTAGCTTTA 300
 AACCCAGACG ATTTGTCTCC AGGGCTGTCA CATCTACTGG CTCTGCCAAG CTTCCGCATG 360
 50 ATCATTGTCT GTGTTTGGAA AGATTATGGA TTAAGTGGTG CTTCTGTTTC TTTTCTGAAT 420
 TTACCAGGAT GTGGAGAACT AGTTTGGGTA GGAGAGCCTC TCACGCTGAG AACAGCAGAA 480
 ACAATTACTG GCAAGTATGG TGTGTGGATG CGAGACCCCA AGCCACCTA CCCCTACACC 540
 55 CAGGAGACCA CGTGGAGAAT CGACACAGTT GGCACGGATG TCCGCCAGGT TTTTGAGTAT 600

GACCTCATCA GCCAGTTTAT GCAGGGCTAC CCTTCTAAGG TTCACATACT GCCTAGGCCA 660
CTGGAAAGCA CGGGTGCTGT GGTGTACTCG GGGAGCCTCT ATTTCCAGGG CGCTGAGTCC 720
5 AGAACTGTCA TAAGATATGA GCTGAATACC GAGACAGTGA AGGCTGAGAA GGAAATCCCT 780
GGAGCTGGCT ACCACGGACA GTTCCCGTAT TCTTGGGGTG GCTACACGGA CATTGACTTG 840
10 GCTGTGGATG AAGCAGGCCT CTGGGTCATT TACAGCACCG ATGAGGCCAA AGGTGCCATT 900
GTCCTCTCCA AACTGAACCC AGAGAATCTG GAACTCGAAC AAACCTGGGA GACAAACATC 960
CGTAAGCAGT CAGTCGCCAA TGCCTTCATC ATCTGTGGCA CCTTGTACAC CGTCAGCAGC 1020
15 TACACCTCAG CAGATGCTAC CGTCAACTTT GCTTATGACA CAGGCACAGG TATCAGCAAG 1080
ACCCTGACCA TCCCATTCAA GAACCGCTAT AAGTACAGCA GCATGATTGA CTACAACCCC 1140
CTGGAGAAGA AGCTCTTTGC CTGGGACAAC TTGAACATGG TCACTTATGA CATCAAGCTC 1200
20 TCCAAGATGT GAAAAGCCTC CAAGCTGTAC AGGCAATGGC AGAAGGAGAT GCTCAGGGCT 1260
CCTGGGGGGA GCAGGCTGAA GGGAGAGCCA GCCAGCCAGG GCCCAGGCAG CTTTGACTGC 1320
25 TTTCCAAGTT TTCATTAATC CAGAAGGATG AACATGGTCA CCATCTAACT ATTCAGGAAT 1380
TGTA GTCTGA GGGCGTAGAC AATTTTCATAT AATAAATATC CTTTATCTTC TGTCAGCATT 1440
TATGGGATGT TTAATGACAT AGTTCAAGTT TTCTTGTGAT TTGGGGCAA AGCTGTAAGG 1500
30 CATAATAGTT TCTTCCTGAA AACCATTGCT CTTGCATGTT ACATGGTTAC CACAAGCCAC 1560
AATAAAAAGC ATAAC TTCTA AAGGAAGCAG AATAGCTCCT CTGGCCAGCA TCGAATATAA 1620
35 GTAAGATGCA TTTACTACAG TTGGCTTCTA ATGCTTCAGA TAGAATACAG TTGGGTCTCA 1680
CATAACCCTT TACATTGTGA AATAAAATTT TCTTACCCAA CGTTCTCTTC CTTGAACTTT 1740
GTGGGAATCT TTGCTTAAGA GAAGGATATA GATTCCAACC ATCAGGTAAT TCCTTCAGGT 1800
40 TGGGAGATGT GATTGCAGGA TGTAAAGGT GGTGTGTGTG TGTGTGTGTG TGTGTGTAAC 1860
TGAGAGGCTT GTGCCTGGTT TTGAGGTGCT GCCCAGGATG ACGCCAAGCA AATAGCAGCA 1920
45 TCCACACTTT CCCACCTCCA TCTCCTGGTG CTCTCGGCAC TACCGGAGCA ATCTTTCCAT 1980
CTCTCCCCTG AACCCACCCT 2000

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2800 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	TACCTGGTAC TTGTTGGCTG GCCAATCTAA CCAAATCAGT GATCCCCAAG CTCAGCGAGA	60
10	CAATCCGTCT CAAAAAACA AAGTGGAGAA TGAAAGAAGA CAACGCCTGA CATAAGCCTC	120
	TAGCTCACAC ACACACACAC ACACACACGC CTATACACAT GAGTGTGCAC CCACCCAGGT	180
15	GAACGCAGAT GCACACATAC CCCACCCACA CAAGAATGGA TTTAGAGCAA GAGGCACTTG	240
	CTCAGTCTTC AGGCGAATCT GCTATGGGAA CATCAGAGAA ATTTATCACA CAGATATCAC	300
	AAATGCTATT ATTAGTATCT GAGAACCAAG TTGCTCAAAT GCAAATGTTG CTCTAAGGAA	360
20	CCCATGAGGG GGCAGTGAGG TGGCTGAGAG GGGGAGGTGC TTAGTGAGCA GGCCTTACAG	420
	ACTGAGGTCA GTCCCTAAAG CCCATGCCAG GAGGAGAGAA CTGGACCCCA AAAGTTGTCC	480
25	TCTGACCACA ACACGGCATG CATGGCCCAT GTGTGCTCAT ATACCCCCCA TATGAGCACA	540
	CACCAGTAAG TAAACATTTA TAAAGATGTT CATGAGGCTT CCACGCACAC ACTGGCTTAT	600
	GTGAACTTCT GACAAGCCTT GGTACTTGGT ACTTGGTTCT CCTGCTTGGT TTTGGTTTTT	660
30	TTCATTTATC TTATTTTTTT ATTTGGAGGA AGGTGTGTGT GTGTGTGTGT CTCTCTGTGT	720
	GTGTGTCTGT GTGTGTGTGT GTGTGTTGTT GTTGTGTTG TTGTTGACAG TTTCTTTTTT	780
35	TAGGAGAAGT CTCATTATAC TGCCCAGTTG TTCTTGAAC TTTTTTGAGA CTTAACAATT	840
	CCCTTACATT GCATTCAAAG TAGTGGGCTC TCTTTGAAAA GGGAGTACTA TTAGCTTACA	900
	GCCCGTGAAT TTGAATTAGT AAGTAACTA AATCTCCATT TTCACAACCT TCTCACTCAG	960
40	TTATTTTCATC TCCTCATGGA TAGCTACCTA AACCTAAAGT TATGATAACA ATACCTGTAT	1020
	TTTCATCCCT ATGTTACAGT TGATACAGGT TTCATGAAAT ACTGTGTATA CTCAAAAGTA	1080
45	CTTTAAAATT AAGCCTTATG TTGAATAGCT TATGTAGCAT ACACTTCTGG CATTTAAATA	1140
	TTTTCATATT GCTAACTAAA TAACGTGTTT CTTTGAGTCC TTACGTTTTA TACGTTTGGA	1200
	GTTATCTTTC AGAGGTGGGC ACACAGGTTT CACCCGTAGG GTTTGGGGGG CACACTCATC	1260
50	CTAAAGCCTG GTCCAGAGCA TTGGCACAGG TTCCTGAGAC AAGAGCTGTG GTTAGGGAGC	1320
	TTTTCTGAGG ATGTTACAG GTTTATTCTA AATCTAGGGC AACATCATGT TCTCATCCCC	1380
55	TCTGTAGGAA CCAGGAGCCT GGAGGCATTG GGCTCTCCTT TGGACTCTTC TTCGTCTCTG	1440
	CTACAGGACG TGTCTACTCA GGCATGTCTG TCTCCCTAGT TCCTTATGCT GGTCCAGTGA	1500

AACACAAAAT AGACTTATAT CCCTGTTCAA ACTAGCACAC AACCAGCTTC TCCTGTCAGA 1560
CAAGGTGCGC ATATGTTTAC AAGCACACAC AAACAGACTA GAAACTTAGG GGTTATTATT 1620
5 GGGATGTGGG GTACATGCAC GGGGACTTCT AAAAAGAAAA TAAATTCAAA ATAGCCTCCG 1680
GCACTTTGTT TTAAAGACT CTTGCTGGCA GTGTGAGTGT AATCCTCCTA TCCCCCATG 1740
10 GCTGGTCCAA CCCAGCTTCA TGTGATCACC TCTCCCTCCC TCCACACAGG GCTGGGTCCC 1800
CAGGATATAT AAATGTCTTT GGACTTCAGG CTTGAGCCAG CAGGGCCACC CATCCAGACA 1860
CCTTGCAGGA GAACTTTCCA GAAGAAACCT CACCCAGCCT CCACACTGCT GTCCTTCTCT 1920
15 GCACGCTGCT GCAGCTGTGG TCCCAAGATG CCAGCTCTCC ATCTGCTGTT TCTGGCCTGC 1980
TTGGTGTGGG GAATGGGGGC CAGGACAGCA CAGTTCCGAA AGGCCAATGA TCGGAGTGGC 2040
CGATGCCAAT ACACCTTCAC TGTGGCCAGC CCAATGAAT CTAGCTGCCC AAGGGAGGAC 2100
20 CAGGCCATGT CAGCCATCCA AGACCTTCAG AGAGACAGCA GCATCCAGCA TGCAGACCTA 2160
GAGTCCACCA AGGCCCGGGT CAGATCCCTG GAGAGTCTCC TCCACCAGAT GACCTTGGGC 2220
25 CGAGTTACTG GGACCCAGGA GGCCCAAGAG GGGCTGCAGG GCCAGTTGGG TGCCCTGAGG 2280
AGAGAACGGG ACCAGCTGGA GACCCAAACC AGGGATCTGG AGGCAGCCTA TAACAATCTC 2340
CTTCGAGATA AGTCGGCTTT AGAGGAAGAG AAGAGGCAGC TGGAACAAGA GAATGAAGAT 2400
30 TTGGCCAGGA GGCTAGAAAG CAGCAGCGAG GAGGTAACAA GGCTGCGGAG GGGCCAGTGT 2460
CCTTCCACCC AGTACCCCTC TCAGGACATG CTGCCAGGCT CCAGGGAAGG TAAGAGTGCA 2520
35 GGGTGGAGTG GCCACCTGAC CCAGAAGGTA GCAAGTTTGC TGGTGACCCA TTACAGGACC 2580
CCCAGGCTTC TCCTTCTGTT TTGTCTTTTC TCTCAGAAAC TGCAAATCCA GCATGCAGTA 2640
40 GTTTCATTAA GGAGAGCAAA GCAAACACTT TTGCATGCTT CTAGAAAGTT GGCTCCTTGT 2700
TTAGGTCAGT GGATCTGAGC TCTTGTGCCC AGTCATGACA AAATGATCAT GGCCACAGC 2760
CAAATGACAA ACATGGGGCC AGGTGGCAGA TACATATGAT 2800

45 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 680 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5 AAGCTTTTTTA ATTATGCCAA TTTCTCCCCG ATTGAGACCA TCACCCTAGT TCCAATGAGC 60
TACCAACGTG GTTCAGTCAT GTTACATCTT CAGATAACAA GTATTTGGGA ACATATCAAA 120
CATCACCCCTC CACAGAGTCC GTTCTTGTC CCTTTCTACT ACAAGTGCCA ATTTTTTCTC 180
TCTTTGAATA CAGTCTCTCA GTGGAATTTG GACACGTTGG CCTTCCAGGA ATTGAAGTCA 240
10 GAGTTAACTG AGGTTCCCTGC TTCCCAAATC TTGAAGGAAA ATCCATCTGG CCGACCCAGG 300
AGCAAAGAAG GAGACAAAGG TATGAAGTTA GACTTCTCCC TTTTGAGCCT ACCTGGCCTC 360
15 CTCTCCCTCT CTCCCTCTCT CCCTCTCTCC CTCTCTCCCT CTCTCCCTCT CTCCCTCTCT 420
CCCTCTCTCC CCTCTCCCCT CCCCCTCTCC CTCCCTGTGT GTGTGTGTGA GTGCATGTAT 480
ATGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGCAT GTGCGTGTGC ATGTATACCT 540
20 TGTTCTGTGT TCAGTTCGGA AAGAGCAACT GTTCACCCAG AAGAGAAGAC AGGTGATTCC 600
CCAAGGCAGA GTTGGGGAGA AGGAAGCTGA AACCTGTCTG CTGCCTTTTC TAGACATATG 660
25 TACTGGAAGC CAACCTTGGA 680

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1456 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

40 CTTTGTCTAT CAAGGAAAAG AGCATTGTG CCTCAAAAAA AAAAAAAAAA AAAAGTGTTT 60
GATAGAAATA TGGCTGCTGT TTCCAGAAAA TAACATTGAC TGTTTATTATTA GCAATCCCTG 120
45 CTAACACTGA AGTCTATGTA GAGGCTAACA CGGAAGGGTA TGTTGAGGGG ATCCGACACC 180
CTCACACAGA CATACTGCA GGCAAAACAC CAATGCACAC AAAAGAAAAA CAAATGAGAA 240
50 AGTCAAGGCT CACAGAGCTA AGTACCTCAC TGGTCACATG GTCAGTGGGC AGCGGGGTTC 300
AGAGGTCAAC CCACTCTGTC TCTGCCTTCT CTGTTTTGCC ACTACTGTCC AGTCTGCAGT 360
CTGTATTTCG AAGACATAGA TACTAAATAC ATGGCAACTC TTTTTTTTGT TTGTTTTAAT 420
55 TCATCAGGAT GTGGAGCGCT AGTCTGGGTA GGAGAGCCAG TCACCCTGAG GACAGCTGAA 480

ACAATCGCTG GCAAGTATGG AGTGTGGATG AGAGACCCCA AGCCCACCCA CCCCTACACC 540
CAGGAAAGCA CATGGAGGAT TGACACGGTT GGCACAGAGA TCCGCCAGGT GTTTGAGTAC 600
5 AGTCAGATAA GCCAGTTCGA GCAGGGCTAT CTTTCCAAGG TCCATGTGCT CCCTCGGGCA 660
CTGGAGAGCA CGGGTGCTGT GGTGTATGCG GGGAGCCTCT ATTTCCAGGG GGCTGAGTCC 720
10 AGAACTGTGG TCAGGTATGA GCTAGACACG GAGACCGTGA AGGCAGAGAA GGAAATTCCT 780
GGAGCTGGCT ACCACGGACA CTTCCCGTAC GCGTGGGGTG GCTACACAGA CATTGACTTA 840
GCTGTGGATG AGAGCGGCCT CTGGGTCATC TACAGCACGG AGGAAGCCAA GGGGGCCATA 900
15 GTCCTCTCCA AATTGAACCC AGCGAACCTG GAACTTGAGC GTACCTGGGA GACTAACATC 960
CGTAAGCAGT CTGTGGCCAA TGCCTTTGTT ATCTGTGGCA TCTTGTACAC GGTGAGCAGC 1020
TACTCTTCAG CCCATGCAAC CGTCAACTTC GCCTACGACA CTAAAACGGG GACCAGTAAG 1080
20 ACCCTGACCA TCCCATTAC GAATCGCTAC AAGTACAGCA GTATGATTGA CTACAACCCC 1140
CTGGAGAGGA AGCTGTTTGC CTGGGACAAC TTCAACATGG TCACCTATGA TATCAAGCTC 1200
25 TTGGAGATGT GAGGAGCCTC TATGCCTACC AGCAAAGGCC AGAAAAGGTG AAGTTCCGGG 1260
CTCCCGGGTG AAGCAGCTGT CAGCAGAGGC AGCCAGATGC ATGGAGTTTC TCCTCCTGCT 1320
AAAGATTTTG TTTATCCGGG TCAATGTACA GCTAGCTCCC CTCTGACTGA CACGTCTCTC 1380
30 AGGCTTGAT AGTCGCATAG ACTCTGTTCT CTTCTGTCAG CTTTCAAAGG GCTGTTCTC 1440
TTTTAAAAAT CACATA 1456

35 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1515 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

45

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..1512

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

55 ATG AGG TTC TTC TGT GCA CGT TGC TGC AGC TTT GGG CCT GAG ATG CCA 48
Met Arg Phe Phe Cys Ala Arg Cys Cys Ser Phe Gly Pro Glu Met Pro
1 5 10 15

	GCT GTC CAG CTG CTG CTT CTG GCC TGC CTG GTG TGG GAT GTG GGG GCC	96
	Ala Val Gln Leu Leu Leu Leu Ala Cys Leu Val Trp Asp Val Gly Ala	
	20 25 30	
5	AGG ACA GCT CAG CTC AGG AAG GCC AAT GAC CAG AGT GGC CGA TGC CAG	144
	Arg Thr Ala Gln Leu Arg Lys Ala Asn Asp Gln Ser Gly Arg Cys Gln	
	35 40 45	
10	TAT ACC TTC AGT GTG GCC AGT CCC AAT GAA TCC AGC TGC CCA GAG CAG	192
	Tyr Thr Phe Ser Val Ala Ser Pro Asn Glu Ser Ser Cys Pro Glu Gln	
	50 55 60	
15	AGC CAG GCC ATG TCA GTC ATC CAT AAC TTA CAG AGA GAC AGC AGC ACC	240
	Ser Gln Ala Met Ser Val Ile His Asn Leu Gln Arg Asp Ser Ser Thr	
	65 70 75 80	
20	CAA CGC TTA GAC CTG GAG GCC ACC AAA GCT CGA CTC AGC TCC CTG GAG	288
	Gln Arg Leu Asp Leu Glu Ala Thr Lys Ala Arg Leu Ser Ser Leu Glu	
	85 90 95	
25	AGC CTC CTC CAC CAA TTG ACC TTG GAC CAG GCT GCC AGG CCC CAG GAG	336
	Ser Leu Leu His Gln Leu Thr Leu Asp Gln Ala Ala Arg Pro Gln Glu	
	100 105 110	
30	ACC CAG GAG GGG CTG CAG AGG GAG CTG GGC ACC CTG AGG CGG GAG CGG	384
	Thr Gln Glu Gly Leu Gln Arg Glu Leu Gly Thr Leu Arg Arg Glu Arg	
	115 120 125	
35	GAC CAG CTG GAA ACC CAA ACC AGA GAG TTG GAG ACT GCC TAC AGC AAC	432
	Asp Gln Leu Glu Thr Gln Thr Arg Glu Leu Glu Thr Ala Tyr Ser Asn	
	130 135 140	
40	CTC CTC CGA GAC AAG TCA GTT CTG GAG GAA GAG AAG AAG CGA CTA AGG	480
	Leu Leu Arg Asp Lys Ser Val Leu Glu Glu Glu Lys Lys Arg Leu Arg	
	145 150 155 160	
45	CAA GAA AAT GAG AAT CTG GCC AGG AGG TTG GAA AGC AGC AGC CAG GAG	528
	Gln Glu Asn Glu Asn Leu Ala Arg Arg Leu Glu Ser Ser Ser Gln Glu	
	165 170 175	
50	GTA GCA AGG CTG AGA AGG GGC CAG TGT CCC CAG ACC CGA GAC ACT GCT	576
	Val Ala Arg Leu Arg Arg Gly Gln Cys Pro Gln Thr Arg Asp Thr Ala	
	180 185 190	
55	CGG GCT GTG CCA CCA GGC TCC AGA GAA GTT TCT ACG TGG AAT TTG GAC	624
	Arg Ala Val Pro Pro Gly Ser Arg Glu Val Ser Thr Trp Asn Leu Asp	
	195 200 205	
60	ACT TTG GCC TTC CAG GAA CTG AAG TCC GAG CTA ACT GAA GTT CCT GCT	672
	Thr Leu Ala Phe Gln Glu Leu Lys Ser Glu Leu Thr Glu Val Pro Ala	
	210 215 220	
65	TCC CGA ATT TTG AAG GAG AGC CCA TCT GGC TAT CTC AGG AGT GGA GAG	720
	Ser Arg Ile Leu Lys Glu Ser Pro Ser Gly Tyr Leu Arg Ser Gly Glu	
	225 230 235 240	

	GGA GAC ACC GGA TGT GGA GAA CTA GTT TGG GTA GGA GAG CCT CTC ACG	768
	Gly Asp Thr Gly Cys Gly Glu Leu Val Trp Val Gly Glu Pro Leu Thr	
	245 250 255	
5	CTG AGA ACA GCA GAA ACA ATT ACT GGC AAG TAT GGT GTG TGG ATG CGA	816
	Leu Arg Thr Ala Glu Thr Ile Thr Gly Lys Tyr Gly Val Trp Met Arg	
	260 265 270	
10	GAC CCC AAG CCC ACC TAC CCC TAC ACC CAG GAG ACC ACG TGG AGA ATC	864
	Asp Pro Lys Pro Thr Tyr Pro Tyr Thr Gln Glu Thr Trp Arg Ile	
	275 280 285	
15	GAC ACA GTT GGC ACG GAT GTC CGC CAG GTT TTT GAG TAT GAC CTC ATC	912
	Asp Thr Val Gly Thr Asp Val Arg Gln Val Phe Glu Tyr Asp Leu Ile	
	290 295 300	
20	AGC CAG TTT ATG CAG GGC TAC CCT TCT AAG GTT CAC ATA CTG CCT AGG	960
	Ser Gln Phe Met Gln Gly Tyr Pro Ser Lys Val His Ile Leu Pro Arg	
	305 310 315 320	
	CCA CTG GAA AGC ACG GGT GCT GTG GTG TAC TCG GGG AGC CTC TAT TTC	1008
	Pro Leu Glu Ser Thr Gly Ala Val Val Tyr Ser Gly Ser Leu Tyr Phe	
	325 330 335	
25	CAG GGC GCT GAG TCC AGA ACT GTC ATA AGA TAT GAG CTG AAT ACC GAG	1056
	Gln Gly Ala Glu Ser Arg Thr Val Ile Arg Tyr Glu Leu Asn Thr Glu	
	340 345 350	
30	ACA GTG AAG GCT GAG AAG GAA ATC CCT GGA GCT GGC TAC CAC GGA CAG	1104
	Thr Val Lys Ala Glu Lys Glu Ile Pro Gly Ala Gly Tyr His Gly Gln	
	355 360 365	
35	TTC CCG TAT TCT TGG GGT GGC TAC ACG GAC ATT GAC TTG GCT GTG GAT	1152
	Phe Pro Tyr Ser Trp Gly Gly Tyr Thr Asp Ile Asp Leu Ala Val Asp	
	370 375 380	
40	GAA GCA GGC CTC TGG GTC ATT TAC AGC ACC GAT GAG GCC AAA GGT GCC	1200
	Glu Ala Gly Leu Trp Val Ile Tyr Ser Thr Asp Glu Ala Lys Gly Ala	
	385 390 395 400	
	ATT GTC CTC TCC AAA CTG AAC CCA GAG AAT CTG GAA CTC GAA CAA ACC	1248
	Ile Val Leu Ser Lys Leu Asn Pro Glu Asn Leu Glu Leu Glu Gln Thr	
	405 410 415	
45	TGG GAG ACA AAC ATC CGT AAG CAG TCA GTC GCC AAT GCC TTC ATC ATC	1296
	Trp Glu Thr Asn Ile Arg Lys Gln Ser Val Ala Asn Ala Phe Ile Ile	
	420 425 430	
50	TGT GGC ACC TTG TAC ACC GTC AGC AGC TAC ACC TCA GCA GAT GCT ACC	1344
	Cys Gly Thr Leu Tyr Thr Val Ser Ser Tyr Thr Ser Ala Asp Ala Thr	
	435 440 445	
55	GTC AAC TTT GCT TAT GAC ACA GGC ACA GGT ATC AGC AAG ACC CTG ACC	1392
	Val Asn Phe Ala Tyr Asp Thr Gly Thr Gly Ile Ser Lys Thr Leu Thr	
	450 455 460	

ATC CCA TTC AAG AAC CGC TAT AAG TAC AGC AGC ATG ATT GAC TAC AAC 1440
 Ile Pro Phe Lys Asn Arg Tyr Lys Tyr Ser Ser Met Ile Asp Tyr Asn
 465 470 475 480

5 CCC CTG GAG AAG AAG CTC TTT GCC TGG GAC AAC TTG AAC ATG GTC ACT 1488
 Pro Leu Glu Lys Lys Leu Phe Ala Trp Asp Asn Leu Asn Met Val Thr
 485 490 495

10 TAT GAC ATC AAG CTC TCC AAG ATG TGA
 1515
 Tyr Asp Ile Lys Leu Ser Lys Met
 500

15 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 504 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

25 Met Arg Phe Phe Cys Ala Arg Cys Cys Ser Phe Gly Pro Glu Met Pro
 1 5 10 15
 30 Ala Val Gln Leu Leu Leu Ala Cys Leu Val Trp Asp Val Gly Ala
 20 25 30
 Arg Thr Ala Gln Leu Arg Lys Ala Asn Asp Gln Ser Gly Arg Cys Gln
 35 35 40 45
 Tyr Thr Phe Ser Val Ala Ser Pro Asn Glu Ser Ser Cys Pro Glu Gln
 50 55 60
 Ser Gln Ala Met Ser Val Ile His Asn Leu Gln Arg Asp Ser Ser Thr
 40 65 70 75 80
 Gln Arg Leu Asp Leu Glu Ala Thr Lys Ala Arg Leu Ser Ser Leu Glu
 85 90 95
 Ser Leu Leu His Gln Leu Thr Leu Asp Gln Ala Ala Arg Pro Gln Glu
 45 100 105 110
 Thr Gln Glu Gly Leu Gln Arg Glu Leu Gly Thr Leu Arg Arg Glu Arg
 115 120 125
 50 Asp Gln Leu Glu Thr Gln Thr Arg Glu Leu Glu Thr Ala Tyr Ser Asn
 130 135 140
 55 Leu Leu Arg Asp Lys Ser Val Leu Glu Glu Glu Lys Lys Arg Leu Arg
 145 150 155 160

Gln Glu Asn Glu Asn Leu Ala Arg Arg Leu Glu Ser Ser Ser Gln Glu
 165 170 175
 5 Val Ala Arg Leu Arg Arg Gly Gln Cys Pro Gln Thr Arg Asp Thr Ala
 180 185 190
 Arg Ala Val Pro Pro Gly Ser Arg Glu Val Ser Thr Trp Asn Leu Asp
 195 200 205
 10 Thr Leu Ala Phe Gln Glu Leu Lys Ser Glu Leu Thr Glu Val Pro Ala
 210 215 220
 Ser Arg Ile Leu Lys Glu Ser Pro Ser Gly Tyr Leu Arg Ser Gly Glu
 225 230 235 240
 15 Gly Asp Thr Gly Cys Gly Glu Leu Val Trp Val Gly Glu Pro Leu Thr
 245 250 255
 20 Leu Arg Thr Ala Glu Thr Ile Thr Gly Lys Tyr Gly Val Trp Met Arg
 260 265 270
 Asp Pro Lys Pro Thr Tyr Pro Tyr Thr Gln Glu Thr Thr Trp Arg Ile
 275 280 285
 25 Asp Thr Val Gly Thr Asp Val Arg Gln Val Phe Glu Tyr Asp Leu Ile
 290 295 300
 Ser Gln Phe Met Gln Gly Tyr Pro Ser Lys Val His Ile Leu Pro Arg
 305 310 315 320
 30 Pro Leu Glu Ser Thr Gly Ala Val Val Tyr Ser Gly Ser Leu Tyr Phe
 325 330 335
 35 Gln Gly Ala Glu Ser Arg Thr Val Ile Arg Tyr Glu Leu Asn Thr Glu
 340 345 350
 Thr Val Lys Ala Glu Lys Glu Ile Pro Gly Ala Gly Tyr His Gly Gln
 355 360 365
 40 Phe Pro Tyr Ser Trp Gly Gly Tyr Thr Asp Ile Asp Leu Ala Val Asp
 370 375 380
 Glu Ala Gly Leu Trp Val Ile Tyr Ser Thr Asp Glu Ala Lys Gly Ala
 385 390 395 400
 45 Ile Val Leu Ser Lys Leu Asn Pro Glu Asn Leu Glu Leu Glu Gln Thr
 405 410 415
 50 Trp Glu Thr Asn Ile Arg Lys Gln Ser Val Ala Asn Ala Phe Ile Ile
 420 425 430
 Cys Gly Thr Leu Tyr Thr Val Ser Ser Tyr Thr Ser Ala Asp Ala Thr
 435 440 445
 55 Val Asn Phe Ala Tyr Asp Thr Gly Thr Gly Ile Ser Lys Thr Leu Thr

450 455 460

Ile Pro Phe Lys Asn Arg Tyr Lys Tyr Ser Ser Met Ile Asp Tyr Asn
 465 470 475 480

5 Pro Leu Glu Lys Lys Leu Phe Ala Trp Asp Asn Leu Asn Met Val Thr
 485 490 495

10 Tyr Asp Ile Lys Leu Ser Lys Met
 500

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1473 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..1470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

30 ATG CCA GCT CTC CAT CTG CTG TTT CTG GCC TGC TTG GTG TGG GGA ATG 48
 Met Pro Ala Leu His Leu Leu Phe Leu Ala Cys Leu Val Trp Gly Met
 1 5 10 15

35 GGG GCC AGG ACA GCA CAG TTC CGA AAG GCC AAT GAT CGG AGT GGC CGA 96
 Gly Ala Arg Thr Ala Gln Phe Arg Lys Ala Asn Asp Arg Ser Gly Arg
 20 25 30

40 TGC CAA TAC ACC TTC ACT GTG GCC AGC CCC AAT GAA TCT AGC TGC CCA 144
 Cys Gln Tyr Thr Phe Thr Val Ala Ser Pro Asn Glu Ser Ser Cys Pro
 35 40 45

45 AGG GAG GAC CAG GCC ATG TCA GCC ATC CAA GAC CTT CAG AGA GAC AGC 192
 Arg Glu Asp Gln Ala Met Ser Ala Ile Gln Asp Leu Gln Arg Asp Ser
 50 55 60

50 AGC ATC CAG CAT GCA GAC CTA GAG TCC ACC AAG GCC CGG GTC AGA TCC 240
 Ser Ile Gln His Ala Asp Leu Glu Ser Thr Lys Ala Arg Val Arg Ser
 65 70 75 80

50 CTG GAG AGT CTC CTC CAC CAG ATG ACC TTG GGC CGA GTT ACT GGG ACC 288
 Leu Glu Ser Leu Leu His Gln Met Thr Leu Gly Arg Val Thr Gly Thr
 85 90 95

55 CAG GAG GCC CAA GAG GGG CTG CAG GGC CAG TTG GGT GCC CTG AGG AGA 336
 Gln Glu Ala Gln Glu Gly Leu Gln Gly Gln Leu Gly Ala Leu Arg Arg
 100 105 110

	GAA CGG GAC CAG CTG GAG ACC CAA ACC AGG GAT CTG GAG GCA GCC TAT	384
	Glu Arg Asp Gln Leu Glu Thr Gln Thr Arg Asp Leu Glu Ala Ala Tyr	
	115 120 125	
5	AAC AAT CTC CTT CGA GAT AAG TCG GCT TTA GAG GAA GAG AAG AGG CAG	432
	Asn Asn Leu Leu Arg Asp Lys Ser Ala Leu Glu Glu Glu Lys Arg Gln	
	130 135 140	
10	CTG GAA CAA GAG AAT GAA GAT TTG GCC AGG AGG CTA GAA AGC AGC AGC	480
	Leu Glu Gln Glu Asn Glu Asp Leu Ala Arg Arg Leu Glu Ser Ser Ser	
	145 150 155 160	
15	GAG GAG GTA ACA AGG CTG CGG AGG GGC CAG TGT CCT TCC ACC CAG TAC	528
	Glu Glu Val Thr Arg Leu Arg Arg Gly Gln Cys Pro Ser Thr Gln Tyr	
	165 170 175	
20	CCC TCT CAG GAC ATG CTG CCA GGC TCC AGG GAA GTC TCT CAG TGG AAT	576
	Pro Ser Gln Asp Met Leu Pro Gly Ser Arg Glu Val Ser Gln Trp Asn	
	180 185 190	
25	TTG GAC ACG TTG GCC TTC CAG GAA TTG AAG TCA GAG TTA ACT GAG GTT	624
	Leu Asp Thr Leu Ala Phe Gln Glu Leu Lys Ser Glu Leu Thr Glu Val	
	195 200 205	
30	CCT GCT TCC CAA ATC TTG AAG GAA AAT CCA TCT GGC CGA CCC AGG AGC	672
	Pro Ala Ser Gln Ile Leu Lys Glu Asn Pro Ser Gly Arg Pro Arg Ser	
	210 215 220	
35	AAA GAA GGA GAC AAA GGA TGT GGA GCG CTA GTC TGG GTA GGA GAG CCA	720
	Lys Glu Gly Asp Lys Gly Cys Gly Ala Leu Val Trp Val Gly Glu Pro	
	225 230 235 240	
40	GTC ACC CTG AGG ACA GCT GAA ACA ATC GCT GGC AAG TAT GGA GTG TGG	768
	Val Thr Leu Arg Thr Ala Glu Thr Ile Ala Gly Lys Tyr Gly Val Trp	
	245 250 255	
45	ATG AGA GAC CCC AAG CCC ACC CAC CCC TAC ACC CAG GAA AGC ACA TGG	816
	Met Arg Asp Pro Lys Pro Thr His Pro Tyr Thr Gln Glu Ser Thr Trp	
	260 265 270	
50	AGG ATT GAC ACG GTT GGC ACA GAG ATC CGC CAG GTG TTT GAG TAC AGT	864
	Arg Ile Asp Thr Val Gly Thr Glu Ile Arg Gln Val Phe Glu Tyr Ser	
	275 280 285	
55	CAG ATA AGC CAG TTC GAG CAG GGC TAT CCT TCC AAG GTC CAT GTG CTC	912
	Gln Ile Ser Gln Phe Glu Gln Gly Tyr Pro Ser Lys Val His Val Leu	
	290 295 300	
60	CCT CGG GCA CTG GAG AGC ACG GGT GCT GTG GTG TAT GCG GGG AGC CTC	960
	Pro Arg Ala Leu Glu Ser Thr Gly Ala Val Val Tyr Ala Gly Ser Leu	
	305 310 315 320	
65	TAT TTC CAG GGG GCT GAG TCC AGA ACT GTG GTC AGG TAT GAG CTA GAC	1008
	Tyr Phe Gln Gly Ala Glu Ser Arg Thr Val Val Arg Tyr Glu Leu Asp	
	325 330 335	

ACG GAG ACC GTG AAG GCA GAG AAG GAA ATT CCT GGA GCT GGC TAC CAC 1056
 Thr Glu Thr Val Lys Ala Glu Lys Glu Ile Pro Gly Ala Gly Tyr His
 340 345 350

5 GGA CAC TTC CCG TAC GCG TGG GGT GGC TAC ACA GAC ATT GAC TTA GCT 1104
 Gly His Phe Pro Tyr Ala Trp Gly Gly Tyr Thr Asp Ile Asp Leu Ala
 355 360 365

10 GTG GAT GAG AGC GGC CTC TGG GTC ATC TAC AGC ACG GAG GAA GCC AAG 1152
 Val Asp Glu Ser Gly Leu Trp Val Ile Tyr Ser Thr Glu Glu Ala Lys
 370 375 380

15 GGG GCC ATA GTC CTC TCC AAA TTG AAC CCA GCG AAC CTG GAA CTT GAG 1200
 Gly Ala Ile Val Leu Ser Lys Leu Asn Pro Ala Asn Leu Glu Leu Glu
 385 390 395 400

20 CGT ACC TGG GAG ACT AAC ATC CGT AAG CAG TCT GTG GCC AAT GCC TTT 1248
 Arg Thr Trp Glu Thr Asn Ile Arg Lys Gln Ser Val Ala Asn Ala Phe
 405 410 415

GTT ATC TGT GGC ATC TTG TAC ACG GTG AGC AGC TAC TCT TCA GCC CAT 1296
 Val Ile Cys Gly Ile Leu Tyr Thr Val Ser Ser Tyr Ser Ser Ala His
 420 425 430

25 GCA ACC GTC AAC TTC GCC TAC GAC ACT AAA ACG GGG ACC AGT AAG ACC 1344
 Ala Thr Val Asn Phe Ala Tyr Asp Thr Lys Thr Gly Thr Ser Lys Thr
 435 440 445

30 CTG ACC ATC CCA TTC ACG AAT CGC TAC AAG TAC AGC AGT ATG ATT GAC 1392
 Leu Thr Ile Pro Phe Thr Asn Arg Tyr Lys Tyr Ser Ser Met Ile Asp
 450 455 460

35 TAC AAC CCC CTG GAG AGG AAG CTG TTT GCC TGG GAC AAC TTC AAC ATG 1440
 Tyr Asn Pro Leu Glu Arg Lys Leu Phe Ala Trp Asp Asn Phe Asn Met
 465 470 475 480

40 GTC ACC TAT GAT ATC AAG CTC TTG GAG ATG TGA 1473
 Val Thr Tyr Asp Ile Lys Leu Leu Glu Met
 485 490

(2) INFORMATION FOR SEQ ID NO:10:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 490 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

55 Met Pro Ala Leu His Leu Leu Phe Leu Ala Cys Leu Val Trp Gly Met
 1 5 10 15
 Gly Ala Arg Thr Ala Gln Phe Arg Lys Ala Asn Asp Arg Ser Gly Arg

	20	25	30
	Cys Gln Tyr Thr Phe Thr Val Ala Ser Pro Asn Glu Ser Ser Cys Pro		
	35	40	45
5	Arg Glu Asp Gln Ala Met Ser Ala Ile Gln Asp Leu Gln Arg Asp Ser		
	50	55	60
10	Ser Ile Gln His Ala Asp Leu Glu Ser Thr Lys Ala Arg Val Arg Ser		
	65	70	75
	Leu Glu Ser Leu Leu His Gln Met Thr Leu Gly Arg Val Thr Gly Thr		
	85	90	95
15	Gln Glu Ala Gln Glu Gly Leu Gln Gly Gln Leu Gly Ala Leu Arg Arg		
	100	105	110
	Glu Arg Asp Gln Leu Glu Thr Gln Thr Arg Asp Leu Glu Ala Ala Tyr		
	115	120	125
20	Asn Asn Leu Leu Arg Asp Lys Ser Ala Leu Glu Glu Glu Lys Arg Gln		
	130	135	140
25	Leu Glu Gln Glu Asn Glu Asp Leu Ala Arg Arg Leu Glu Ser Ser Ser		
	145	150	155
	Glu Glu Val Thr Arg Leu Arg Arg Gly Gln Cys Pro Ser Thr Gln Tyr		
	165	170	175
30	Pro Ser Gln Asp Met Leu Pro Gly Ser Arg Glu Val Ser Gln Trp Asn		
	180	185	190
	Leu Asp Thr Leu Ala Phe Gln Glu Leu Lys Ser Glu Leu Thr Glu Val		
	195	200	205
35	Pro Ala Ser Gln Ile Leu Lys Glu Asn Pro Ser Gly Arg Pro Arg Ser		
	210	215	220
40	Lys Glu Gly Asp Lys Gly Cys Gly Ala Leu Val Trp Val Gly Glu Pro		
	225	230	235
	Val Thr Leu Arg Thr Ala Glu Thr Ile Ala Gly Lys Tyr Gly Val Trp		
	245	250	255
45	Met Arg Asp Pro Lys Pro Thr His Pro Tyr Thr Gln Glu Ser Thr Trp		
	260	265	270
	Arg Ile Asp Thr Val Gly Thr Glu Ile Arg Gln Val Phe Glu Tyr Ser		
	275	280	285
50	Gln Ile Ser Gln Phe Glu Gln Gly Tyr Pro Ser Lys Val His Val Leu		
	290	295	300
55	Pro Arg Ala Leu Glu Ser Thr Gly Ala Val Val Tyr Ala Gly Ser Leu		
	305	310	315
			320

Tyr Phe Gln Gly Ala Glu Ser Arg Thr Val Val Arg Tyr Glu Leu Asp
 325 330 335
 5 Thr Glu Thr Val Lys Ala Glu Lys Glu Ile Pro Gly Ala Gly Tyr His
 340 345 350
 Gly His Phe Pro Tyr Ala Trp Gly Gly Tyr Thr Asp Ile Asp Leu Ala
 355 360 365
 10 Val Asp Glu Ser Gly Leu Trp Val Ile Tyr Ser Thr Glu Glu Ala Lys
 370 375 380
 Gly Ala Ile Val Leu Ser Lys Leu Asn Pro Ala Asn Leu Glu Leu Glu
 385 390 395 400
 15 Arg Thr Trp Glu Thr Asn Ile Arg Lys Gln Ser Val Ala Asn Ala Phe
 405 410 415
 Val Ile Cys Gly Ile Leu Tyr Thr Val Ser Ser Tyr Ser Ser Ala His
 420 425 430
 Ala Thr Val Asn Phe Ala Tyr Asp Thr Lys Thr Gly Thr Ser Lys Thr
 435 440 445
 25 Leu Thr Ile Pro Phe Thr Asn Arg Tyr Lys Tyr Ser Ser Met Ile Asp
 450 455 460
 Tyr Asn Pro Leu Glu Arg Lys Leu Phe Ala Trp Asp Asn Phe Asn Met
 465 470 475 480
 30 Val Thr Tyr Asp Ile Lys Leu Leu Glu Met
 485 490

(2) INFORMATION FOR SEQ ID NO:11:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA (genomic)

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGGGCTGCA GAGGGAGCTG GGCACCCTG

29

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(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

55

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

10

ATACTGCCTA GGCCACTGGA

20

(2) INFORMATION FOR SEQ ID NO:13:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

30

CAATGTCCGT GTAGCCACC

19

(2) INFORMATION FOR SEQ ID NO:14:

35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAACTCGAAC AAACCTGGGA

20

(2) INFORMATION FOR SEQ ID NO:15:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CATGCTGCTG TACTTATAGC GG

22

10

- (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCTGGCTCC CCAGTATATA

20

- (2) INFORMATION FOR SEQ ID NO:17:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

40

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACAGCTGGCA TCTCAGGC

18

- (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

55

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 18
ACGTTGCTCC AGCTTTGG

(2) INFORMATION FOR SEQ ID NO:19:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19: 19
GATGACTGAC ATGGCCTGG

25 (2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
35 (A) DESCRIPTION: /desc = "primer"

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20: 20
AGTGGCCGAT GCCAGTATAC

(2) INFORMATION FOR SEQ ID NO:21:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTGGTCCAAG GTCAATTGGT

20

5 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15 (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

20

AGGCCATGTC AGTCATCCAT

20

(2) INFORMATION FOR SEQ ID NO:23:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCTCTGGTTT GGGTTTCCAG

20

40

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

45

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

50

(A) DESCRIPTION: /desc = "primer"

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGACCTTGGA CCAGGCTG

18

(2) INFORMATION FOR SEQ ID NO:25:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCTGGCCAGA TTCTCATTTT

20

20

(2) INFORMATION FOR SEQ ID NO:26:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGAGGAAGA GAAGAAGCGA

20

40

(2) INFORMATION FOR SEQ ID NO:27:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

55

CTGCTGAACT CAGAGTCCCC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AACATAGTCA ATCCTTGGGC C

21

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TAAAGACCAT GTGGGCACAA

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTATGGATTA AGTGGTGCTT CG

22

(2) INFORMATION FOR SEQ ID NO:31:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

15 ATTCTCCACG TGGTCTCCTG 20

(2) INFORMATION FOR SEQ ID NO:32:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AAGCCACCT ACCCCTACAC 20

35 (2) INFORMATION FOR SEQ ID NO:33:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

50 AATAGAGGCT CCCCAGGTAC A 21

(2) INFORMATION FOR SEQ ID NO:34:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
ATACTGCCTA GGCCACTGGA 20

15 (2) INFORMATION FOR SEQ ID NO:35:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"
25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
30 CAATGTCCGT GTAGCCACC 19

(2) INFORMATION FOR SEQ ID NO:36:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
40 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"
45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
TGGCTACCCAC GGACACTTC 19

50 (2) INFORMATION FOR SEQ ID NO:37:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
55 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

10 CATTGGCGAC TGACTGCTTA 20

(2) INFORMATION FOR SEQ ID NO:38:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

30 GAACTCGAAC AAACCTGGGA 20

(2) INFORMATION FOR SEQ ID NO:39:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CATGCTGCTG TACTTATAGC GG 22

(2) INFORMATION FOR SEQ ID NO:40:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

55 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGCAAGACCC TGACCATCC

19

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- (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

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- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AGCATCTCCT TCTGCCATTG

20

30

- (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

40

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

45

TTCCTTCAGG TTGGGAGATG

20

50

- (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

5

GAGAGCACCA GGAGATGGAG

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12Q 1/68	A3	(11) International Publication Number: WO 99/51779 (43) International Publication Date: 14 October 1999 (14.10.99)
(21) International Application Number: PCT/US99/07671 (22) International Filing Date: 7 April 1999 (07.04.99) (30) Priority Data: 09/056,285 7 April 1998 (07.04.98) US (71) Applicant: THE UNIVERSITY OF IOWA RESEARCH FOUNDATION [US/US]; 214 Technology Innovation Center, Oakdale Research Campus, Iowa City, IA 52319 (US). (72) Inventors: STONE, Edwin, M.; 534 Woodridge Avenue, Iowa City, IA 52242 (US). SHEFFIELD, Val, C.; 13 Oak Park Place, N.E., Coralville, IA 52240 (US). ALWARD, Wallace, L., M.; 2015 Ridgeway Drive, Iowa City, IA 52245 (US). FINGERT, John; 481 Wetwinds Drive, Iowa City, IA 52246 (US). (74) Agents: ARNOLD, Beth, E. et al.; Foley, Hoag & Eliot, LLP, One Post Office Square, Boston, MA 02109 (US).		(81) Designated States: AU, BR, CA, JP, MX, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims</i> <i>and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 29 December 1999 (29.12.99)
(54) Title: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS (57) Abstract Methods and compositions for preventing and treating glaucoma; and glaucoma diagnostics are disclosed.		

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/07671

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	STONE E.M. ET AL.: "Identification of a gene that causes primary open angle glaucoma" SCIENCE, vol. 275, 1997, pages 668-670, XP002049424 US the whole document	1-13
X	KUBOTA R. ET AL.: "Genomic organisation of the human myocilin gene (MYOC) responsible for primary open angle glaucoma" BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 242, 1998, pages 396-400, XP002120488 US the whole document	1-13

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

28 October 1999

Date of mailing of the international search report

16/11/1999

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Authorized officer

Luzzatto, E

INTERNATIONAL SEARCH REPORT

Internat. Application No.

PCT/US 99/07671

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	KUBOTA R. ET AL.: "A novel myosin-like protein (myocilin) expressed in the connecting cilium of the photoreceptor: molecular cloning, tissue expression, and chromosomal mapping" GENOMICS, vol. 41, no. 3, 1 May 1997 (1997-05-01), pages 360-369, XP002120489 US the whole document	1-8
X	WO 96 14411 A (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA) 17 May 1996 (1996-05-17) page 36 -page 41; claims; figures	1
P,X	W.L.M. ALWARD ET AL.: "Clinical features associated with mutations in the chromosome 1 open-angle glaucoma gene (GLC1A)" THE NEW ENGLAND JOURNAL OF MEDICINE, vol. 338, 9 April 1998 (1998-04-09), pages 1022-1027, XP002120490 US the whole document	1-13
P,X	WO 98 32850 A (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA) 30 July 1998 (1998-07-30) the whole document	1-8
P,X	WO 98 20131 A (UNIVERSITY OF IOWA) 14 May 1998 (1998-05-14) the whole document esp. table 3	1-13

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 99/07671

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9614411 A	17-05-1996	US 5606043 A	25-02-1997
		AU 2432897 A	22-10-1998
		AU 705420 B	20-05-1999
		AU 4279296 A	31-05-1996
		CA 2204375 A	17-05-1996
		EP 0789762 A	20-08-1997
		JP 10509866 T	29-09-1998
		NO 972024 A	02-07-1997
		NZ 297601 A	29-04-1999
		WO 9844107 A	08-10-1998
		US 5849879 A	15-12-1998
		US 5789169 A	04-08-1998
		US 5861497 A	19-01-1999
		US 5854415 A	29-12-1998
		ZA 9509256 A	14-08-1996
WO 9832850 A	30-07-1998	AU 5820498 A	18-08-1998
WO 9820131 A	14-05-1998	US 5925748 A	20-07-1999
		US 5885776 A	23-03-1999
		AU 5436498 A	29-05-1998
		EP 0942975 A	22-09-1999



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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12Q 1/68	A3	(11) International Publication Number: WO 99/51779 (43) International Publication Date: 14 October 1999 (14.10.99)
(21) International Application Number: PCT/US99/07671 (22) International Filing Date: 7 April 1999 (07.04.99) (30) Priority Data: 09/056,285 7 April 1998 (07.04.98) US (71) Applicant: THE UNIVERSITY OF IOWA RESEARCH FOUNDATION [US/US]; 214 Technology Innovation Center, Oakdale Research Campus, Iowa City, IA 52319 (US). (72) Inventors: STONE, Edwin, M.; 534 Woodridge Avenue, Iowa City, IA 52242 (US). SHEFFIELD, Val, C.; 13 Oak Park Place, N.E., Coralville, IA 52240 (US). ALWARD, Wallace, L., M.; 2015 Ridgeway Drive, Iowa City, IA 52245 (US). FINGERT, John; 481 Wetwinds Drive, Iowa City, IA 52246 (US). (74) Agents: ARNOLD, Beth, E. et al.; Foley, Hoag & Eliot, LLP, One Post Office Square, Boston, MA 02109 (US).		(81) Designated States: AU, BR, CA, JP, MX, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 29 December 1999 (29.12.99)
(54) Title: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS (57) Abstract Methods and compositions for preventing and treating glaucoma; and glaucoma diagnostics are disclosed.		

*(Referred to in PCT Gazette No. 7/2000, Section II)

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CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

Glaucoma Therapeutics and Diagnostics

5

1. Background of the Invention

Glaucoma is an optic nerve disorder characterized by cupping of the optic nerve head and loss of peripheral vision. Occasionally there is also loss of central vision. In the majority of patients, an elevated intraocular pressure is present and is thought to contribute to the optic nerve damage. Glaucoma is the second leading cause of blindness in developed countries (Leske, M.C. (1983) *Am. J. of Epidemiology* 118:166-191). Its prevalence increases with age and is greater in black patients (Leske, M.C. (1983) *Am. J. of Epidemiology* 118:166-191). Glaucoma affects approximately 2.3 million Americans and blinds approximately 12,000 of them per year (Tielsch, J.M. (1993) Therapy for glaucoma: costs and consequences. In *Transactions of the New Orleans Academy of Ophthalmologists*, S.F. Ball, Franklin, R.M. (Ed.), pp 61-68. Kugler, Amsterdam).

The most prevalent form of glaucoma is primary open angle glaucoma (POAG), a progressive disease of the optic nerve characterized by degeneration and cupping of the optic nerve, loss of peripheral visual field, and increased intra-ocular pressure. Evidence indicates that POAG is genetically heterogeneous with a complex mode of inheritance. An early onset form of POAG known as juvenile open angle glaucoma (JOAG) is an autosomal dominant disorder with high penetrance.

A significant fraction of glaucoma has a genetic basis (Benedict, T.W.G. Abhaundlungen zus dem Gebiete der Augenheilkunde. Breslau: L. Freunde (1842); Stokes, (1940) *W. Arch Ophthalmol* 24:885-909; Kellerman, L. and A. Posner, (1955) *Am. J. Ophthalmol.* ;40:681-685; Becker, B., et al., (1960) *Am. J. Ophthalmol.* 50:557-567; Francois, J., et. al., (1966) *Am. J. Ophthalmol.*;62:1067-1071; Armaly, M.F. (1967) *Arch Ophthalmol*;78:35-43; Davies, T.G.. (1968) *Br. J. Ophthalmol.*:52:31-39; Jay, B., Paterson, G. (1970) *Trans. Ophthalmol. Soc. U.K.*;90:161-171; Paterson, G. (1970) *Trans. Ophthalmol. Soc. U.K.*;90:515-525; Miller, S.J.H. (1978) *Trans. Ophthalmol. Soc.U.K.* 98:290-292), which allows genetic methods to be used to investigate the pathophysiological mechanisms of the disease at the molecular level. The chromosomal locations of genes causing three genetically distinct types of primary open angle glaucoma have been identified (Sheffield, V., et al. (1993) *Nature Genetics* 4:47-50;

Sunden, S.L.F., *et al.* (1996) 6:862-869; Richards, J.E., *et al.* (1994) *Am. J. Hum. Genet.*:54:62-70; Wiggs, J.L., *et al.* (1994) *Genomics*;21:299-303; Stoilova, D., *et al.* (1996) *Genomics* 36:142-150; Wirtz, M.K., *et al.* (1997) *Am. J. Hum. Genet.* 60:296-304).

5 Therapeutics, which modulate (agonize or antagonize) genes (wild-type or mutant) involved in glaucoma, would be useful for the prevention and treatment of glaucoma. In addition, the detection of mutations in genes that correlate with the existence or a predisposition to the development of glaucoma can provide useful
10 diagnostics.

2. Summary of the Invention

 In one aspect, the invention features isolated GLC1A nucleic acid molecules. The disclosed molecules can be non-coding, (e.g. probe, antisense or ribozyme molecules) or can encode a functional polypeptide (e.g. a polypeptide which
15 specifically modulates, e.g., by acting as either an agonist or antagonist, at least one bioactivity of a myocilin polypeptide).

 In further embodiments, the nucleic acid molecule is a GLC1A nucleic acid that is at least 70%, preferably 80%, more preferably 85%, and even more preferably at least 95% homologous in sequence to the nucleic acids shown as SEQ ID
20 No. 7 or 9 or to the complement thereof. In another embodiment, the nucleic acid molecule encodes a polypeptide that is at least 92% and more preferably at least 95% similar in sequence to the polypeptide shown in SEQ ID No: 8 or 10.

 The invention also provides probes and primers comprising substantially purified oligonucleotides, which correspond to a region of nucleotide sequence which
25 hybridizes to at least about 6 consecutive nucleotides of the sequences set forth as SEQ ID Nos: 1, 2, 3, 4, 5 or 6 or complements of the sequences set forth as SEQ ID Nos: 1, 2, 3, 4, 5 or 6 or naturally occurring mutants thereof. In preferred embodiments, the probe/primer further includes a label group attached thereto, which is capable of being detected.

30 For expression, the subject GLC1A nucleic acids can include a transcriptional regulatory sequence, e.g. at least one of a transcriptional promoter (e.g., for constitutive expression or inducible expression) or transcriptional enhancer or suppressor sequence, which regulatory sequence is operably linked to the GLC1A gene sequence. Such regulatory sequences in conjunction with a GLC1A nucleic acid

molecule can provide a useful vector for gene expression. This invention also describes host cells transfected with said expression vector whether prokaryotic or eukaryotic and *in vitro* (e.g. cell culture) and *in vivo* (e.g. transgenic) methods for producing GLC1A proteins by employing said expression vectors.

5 In another aspect, the invention features isolated myocilin polypeptides, preferably substantially pure preparations, e.g. of plasma purified or recombinantly produced myocilin polypeptides. In one embodiment, the polypeptide is identical to or similar to a myocilin protein represented in SEQ ID No: 8 or 10. Related members of the vertebrate and particularly the mammalian myocilin family are also within the scope
10 of the invention. Preferably, a myocilin polypeptide has an amino acid sequence at least about 92% homologous and preferably at least about 95%, 96%, 97%, 98% or 99% homologous to the polypeptide represented in SEQ ID No: 8 or 10. In a preferred embodiment, the myocilin polypeptide is encoded by a nucleic acid which hybridizes with a nucleic acid sequence represented in one of SEQ ID No: 7 or 9. The subject
15 myocilin proteins also include modified proteins, which are resistant to post-translational modification, as for example, due to mutations which alter modification sites (such as tyrosine, threonine, serine or asparagine residues), or which prevent glycosylation of the protein, or which prevent interaction of the protein with intracellular proteins involved in signal transduction.

20 The myocilin polypeptide can comprise a full length protein, such as represented in SEQ ID No: 8 or 10, or it can comprise a fragment corresponding to one or more particular motifs/domains, or to arbitrary sizes, e.g., at least 5, 10, 25, 50, 100, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 460, 470, 475, 480, 485, or 490 amino acids in length.

25 Another aspect of the invention features chimeric molecules (e.g. fusion proteins) comprised of a myocilin protein. For instance, the myocilin protein can be provided as a recombinant fusion protein which includes a second polypeptide portion, e.g., a second polypeptide having an amino acid sequence unrelated (heterologous) to the myocilin polypeptide (e.g. the second polypeptide portion is glutathione-S-
30 transferase, an enzymatic activity such as alkaline phosphatase or an epitope tag).

Yet another aspect of the present invention concerns an immunogen comprising a myocilin polypeptide in an immunogenic preparation, the immunogen being capable of eliciting an immune response specific for a myocilin polypeptide; e.g. a humoral response, an antibody response and/or cellular response. In preferred

embodiments, the immunogen comprises an antigenic determinant, e.g. a unique determinant, from the protein represented in SEQ ID Nos: 8 or 10.

A still further aspect of the present invention features antibodies and antibody preparations specifically reactive with an epitope of the myocilin protein. In preferred embodiments the antibody specifically binds to at least one epitope represented in SEQ ID Nos: 8 or 10.

The invention also features transgenic non-human animals which include (and preferably express) a heterologous form of a GLC1A gene described herein, or which misexpress an endogenous GLC1A gene (e.g., an animal in which expression of one or more of the subject GLC1A proteins is disrupted). Such a transgenic animal can serve as an animal model for studying cellular and tissue disorders comprising mutated or mis-expressed GLC1A alleles or for use in drug screening. Alternatively, such a transgenic animal can be useful for expressing recombinant myocilin polypeptides.

In yet another aspect, the invention provides assays, e.g., for screening test compounds to identify inhibitors, or alternatively, potentiators, of an interaction between a myocilin protein and, for example, a virus, an extracellular ligand of the myocilin protein, or an intracellular protein which binds to the myocilin protein.

A further aspect of the present invention provides a method of determining if a subject is at risk for glaucoma or another disorder resulting from a mutant GLC1A gene. The method includes detecting, in a tissue of the subject, the presence or absence of a genetic lesion characterized by at least one of (i) a mutation of a gene encoding a myocilin protein, (e.g., a gene represented in one of SEQ ID Nos: 7 or 9, or a homolog thereof or a mutation of a GLC1A intronic sequence, e.g. as represented in SEQ ID Nos. 1-6); or (ii) the mis-expression of a GLC1A gene. In preferred embodiments, detecting the genetic lesion includes ascertaining the existence of at least one of: a deletion of one or more nucleotides from a GLC1A gene; an addition of one or more nucleotides to the gene, a substitution of one or more nucleotides of the gene, a gross chromosomal rearrangement of the gene; an alteration in the level of a messenger RNA transcript of the gene (e.g., due to a promoter mutation); the presence of a non-wild type splicing pattern of a messenger RNA transcript of the gene; a non-wild type level of the protein; and/or an aberrant level of soluble myocilin protein.

For example, detecting the genetic lesion can include (i) providing a probe/primer comprised of an oligonucleotide which hybridizes to a sense or antisense sequence of a GLC1A gene or naturally occurring mutants thereof, or intronic flanking

sequences naturally associated with the GLC1A gene; (ii) contacting the probe/primer to an appropriate nucleic acid containing sample; and (iii) detecting, by hybridization of the probe/primer to the nucleic acid, the presence or absence of the genetic lesion; e.g. wherein detecting the lesion comprises utilizing the probe/primer to determine the nucleotide sequence of the GLC1A gene and, optionally, of the flanking nucleic acid sequences. For instance, the primer can be employed in a polymerase chain reaction (PCR) or in a ligation chain reaction (LCR). In alternate embodiments, the level of a GLC1A protein is detected in an immunoassay using an antibody which is specifically immunoreactive with the myocilin protein.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

3. Brief Description of the Figures

Figure 1 is an alignment of human and mouse GLC1A gene sequences. The three exons of the human and mouse GLC1A genes and flanking sequences are aligned in panels A, B and C. These sequences are not continuous. Exon sequences are reported in capital letters while flanking sequences are in lower-case letters. Nucleotides conserved between mouse and human are indicated by a closed circle. In panel 1A, exon 1 and flanking promoter and intron 1 sequences are shown. A subset of putative promoter and enhancer elements are underlined and labeled. GRE half-sites are indicated by "GR". A (CA) repeat polymorphism in the 5' flanking region of the human GLC1A gene is also underlined and labeled "(CA) repeat polymorphism". In panel 1B, exon 2 and flanking intron 1 and intron 2 sequences are shown. In panel 1C, exon 3 and flanking intron 2 and downstream sequences are shown. Polyadenylation signal sequences are underlined and labeled "poly-A". A (CA) repeat polymorphism downstream of the human GLC1A gene is also underlined and labeled "(CA) repeat polymorphism".

Figure 2 is a schematic representation of putative motifs that are conserved between human and mouse myocilin proteins.

Figure 3 is an alignment of the proteins predicted by the mouse and human GLC1A genes. Amino acids conserved between mouse and human are indicated by a closed circle. The location of disease-causing mutations previously identified in the human GLC1A gene are indicated. For each missense mutation, the mutant residue is shown directly above the wild-type amino acid. The location of a nonsense mutation is indicated by a "1" and the location of an insertion mutation is indicated by a "2".

4. Detailed Description of the Invention

4.1. General

5 As reported herein, a genetic locus associated with JOAG was identified on chromosome 1q21-q31 by genetic linkage analysis. Observed recombinations between the glaucoma phenotype and highly polymorphic genetic markers in two large JOAG kindreds allowed the interval containing GLC1A gene to be narrowed to a 3 cM region of chromosome 1q between markers D1S3665 and D1S3664. Further evaluation
10 of marker haplotypes revealed that each of three pairs of glaucoma families shared alleles of the same eight contiguous markers suggesting that the GLC1A gene lies within a narrower interval defined by D1S1619 and D1S3664.

Several genes mapping to the GLC1A region of chromosome 1 were considered as candidates for the disease-causing gene. Three genes (LAMC1 (H.C. Watkins et. al., (1993) *Hum. Mol. Genet.* 2: 1084), NPRI (D.G. Lowe et al., (1990) *Genomics* 8:304), and CNR2 (S. Munro et al., (1993) *Nature* 365:61), were excluded
15 from the candidate region by genetic linkage analysis using intragenic polymorphic markers. Five additional candidate genes were determined to lie within the observed recombinant interval by YAC STS content mapping: selectin E (M.P. Bevilacqua et al., (1989) *Science* 243:1160) (GenBank accession no. M24736); selectin L (T.F. Tedder et al., (1989) *J. Exp. Med.* 170:123) (GenBank accession no. M25280); TXGP-1 (S. Miura et al., (1991) *Mol. Cell Biol* 11:1313) (GenBank accession no. MD90224; APT1LG1 (T. Takahashi et al., (1994) *Int. Immunol.* 6, 1567); and TIGR (Trabecular meshwork
20 Induced Glucocorticoid Response Protein) (J.R. Polansky et al., (1989) *Prog. Clin. Biol. Res* 12:113; J. Escribano et al., (1995) *J. Biochem.* 118:921; *International Patent Application Publication No.* WO 96/14411) (GenBank accession nos. R95491, R95447, R95443, R47209). However, two of these genes (selectin E, and selectin L) were found to lie outside of the shared haplotype interval with this approach. The remaining genes (APT1LG1, TXGP-1, and TIGR) were found to map within the narrowest JOAG
25 interval by both YAC STS content and radiation hybrid mapping.
30

Two of these genes (APT1LG1 and TIGR) were screened for mutations in families with JOAG. Primers were selected from the available sequence (T. Takahashi et al., (1994) *Int. Immunol.* 6; 1567, J. Escribano et al., (1995) *J. Biochem.* 118:921; *International Patent Application Publication No.* WO 96/14411) (GenBank

accession nos. R95491, R95447, R95443, R47209) and overlapping PCR amplification products were evaluated by single strand conformation polymorphism analysis (B.J. Bassam et al., (1991) *Anal. Biochem.* 196: 80) and direct DNA sequencing. Although the complete cDNA sequence of the APT1LG1 and TIGR genes have been published, the presence of intervening sequences permitted only 85 - 90% of their coding sequences to be screened in genomic DNA. Eight unrelated JOAG patients were screened with the APT1LG1 assay but no sequence variants were identified.

The TIGR gene assay was initially used to screen affected members of four different 1q-linked glaucoma families, and affected members of four smaller families implicated by haplotypic data. Amino-acid-altering mutations were detected in four of eight families. A tyrosine to histidine mutation in codon 437 was detected in all 22 affected members of the original family (V.C. Sheffield et al., (1993) *Nature Genet.* 4:47) linked to 1q. A glycine to valine mutation in codon 364 was detected in two families including one previously unreported adult-onset open angle glaucoma family with 15 affected members. A nonsense mutation (glutamine to stop) at codon 368 was detected in two families. The latter mutation would be expected to result in a truncation of the gene product.

The prevalence of mutations in the two PCR amplimers that harbored these three changes was then estimated by screening four different populations: glaucoma patients with a family history of the disease; unselected primary open angle glaucoma probands seen in a single clinic; the general population (approximated by patients with heritable retinal disease and spouses from families who participated in prior linkage studies); and, unrelated volunteers over the age of 40 with normal intraocular pressures and no personal or family history of glaucoma. PCR products determined to contain a sequence variation by SSCP were sequenced and compared to sequence generated from an unaffected individual as well as the normal chromosome in each affected individual. Overall, missense or nonsense mutations were found in about 3-5% of unrelated glaucoma patients and in about 0.2% of controls. A Chi-square test revealed this difference to be significant ($p < 0.001$).

In a subsequent study, SSCP screening followed by sequencing of DNA from 1312 unrelated individuals revealed a total of 33 GLC1A sequence changes. Sequencing of the entire GLC1A coding region amplified from the probands of three families with 1q-linked glaucoma, but without SSCP shifts revealed three additional sequence changes. Sixteen of these 36 sequence variations (Table 1) met the following

criteria for a "probable" disease causing mutation: 1) presence in one or more glaucoma patients; 2) alteration of the predicted amino acid sequence; 3) presence in less than 1% of the general population; 4) absence in the 91 normal volunteers. These sixteen mutations were found in 34 of the 716 glaucoma probands (4.7%). Ten sequence
5 changes failed to alter the predicted amino acid sequence of GLC1A and are therefore likely to be non-disease-causing polymorphisms (Table 3). Nine sequence changes altered the predicted amino acid sequence of GLC1A (eight) or the 5' flanking region (one) but were judged likely to be non-disease-causing polymorphisms (Table 2) for one
10 of the following reasons: they were present in more than 1% of the general population (three), they were found only in the normal or general population (five), or they were found in the same allele as a more likely disease-causing mutation (one).

Table 1
Probable Mutations

5	1) GLN19HIS
	2) ARG82CYS
	3) TRP286ARG
	4) THR293LYS
	5) PRO361SER
	6) GLY364VAL
10	7) GLN368STOP
	8) THR377MET
	9) ASP380GLY
	10) 396INS397
	11) ARG422HIS
15	12) TYR437HIS
	13) ALA445VAL
	14) ARG470CYS
	15) ILE477ASN
	16) LYS500ARG
20	

Table 2
Probable Polymorphism

25	1) GLU352LYS
	2) CYS9SER
	3) ASN73SER
	4) ARG76LYS
	5) LYS398ARG
30	6) ARG422CYS
	7) SER425PRO
	8) TYR473CYS
	9) VAL495ILE7

Table 3
Third Nucleotide (Wobble) Polymorphisms

5	1) PRO13PRO
	2) GLY122GLY
	3) LEU159LEU
	4) LYS266LYS
	5) THR285THR
	6) THR325THR
10	7) VAL329VAL
	8) TYR347TYR
	9) GLU396GLU
	10) VAL439VAL

15 Bacterial artificial chromosomes (BACs) containing the human GLC1A gene and its mouse orthologue were subcloned and sequenced to reveal the genomic structure of the genes. Both the human and mouse GLC1A genes are composed of three exons. Human exon 1 (including the 5' promoter region of exon 1, base pairs 1-1905; exon 1, base pairs 1906-2509; and the 5' end of intron 1, base pairs 2510-2800) is set forth as SEQ ID No: 1. Human exon 2 (including the 3' end of intron 1, base pairs 1-193; exon 2, base pairs 194-319; and the 5' end of intron 2, base pairs 320-680) is set forth as SEQ ID No:2. Human exon 3 (including the 3' end of intron 2, base pairs 1-427; exon 3, base pairs 428-1212; and the 3' UTR, base pairs 1213-2000) is set forth as SEQ ID No:3. Mouse exon 1 (including the 5' promoter region of exon 1; base pairs 1-1947; exon 1, base pairs 1948-2509; and the 5' end of intron 1, base pairs 2510-2800) is set forth as SEQ ID No:4. Mouse exon 2 (including the 3' end of intron 1, base pairs 1-193; exon 2, base pairs 194-319; and the 5' end of intron 2, base pairs 320-680) is set forth as SEQ ID No:5 and mouse exon 3 (including the 3' end of intron 2, base pairs 1-427; exon 3, base pairs 428-1212 and the 3' UTR, base pairs 1213-1456) is set forth as SEQ ID No:6. Exons two and three are 126 base pairs and 782 base pairs long in both genes, while exon one is 604 base pairs in the human gene and 562 base pairs in the mouse gene. Exon-intron borders are completely conserved between mouse and human. The human coding GLC1A nucleotide sequence is comprised of 1512 nucleotides (SEQ ID No: 7) and encodes a 504 amino acid myocilin protein (SEQ ID NO. 8) having a molecular weight of about 57kDa. The mouse coding GLC1A nucleotide sequence is

comprised of 1470 nucleotides (SEQ ID No: 9) and encodes a 490 amino acid myocilin protein (SEQ ID No: 10) having a molecular weight of about 55 kDa. The human and mouse coding sequences are 83% identical at the nucleotide level and predict proteins that are 82% identical at the amino acid level.

5 Many putative transcription regulatory sequences were identified in the upstream region of the GLC1A genes (Table 4). Three poly-adenylation sites were located in the 3' UTR of the human gene at positions 1714, 1864 and 2006 base pairs following the putative start codon. Additionally the human GLC1A gene was found to be closely flanked by two CA simple tandem repeat polymorphisms (STRPs) that
10 proved to be useful genetic markers for tracing the segregation of the gene within families.

Table 4
Putative GLC1A promoter and enhancer elements

15	<u>Human and Mouse</u>	<u>Human only</u>	<u>Mouse only</u>
	AP-1	AFP1	DTF-1
	AP-2	CF2-II	GATA-2
	AP-3	CP2	Hb
20	AR	DBP	Lva
	c-ETS	Elk-1	Lvb-binding factor
	c-Myc	G6 Factor	MAF
	C/EBP	HNF-1	MAZ
	CAC-binding protein	HOX-D8	muEBP-C2
25	Dr	HOX-D9	NF-E2
	En	HOX-10	PTFI-beta
	F2F	IRF	TF3-s
	GATA-1	LyF-1	USF
	GFII	MBF-1	
30	GR	MCBF	
	HiNF-A	Myogenin	

	<u>Human and Mouse</u>	<u>Human only</u>
	HNF-3	NF-InsE
	MBF-1	TCF-2alpha
5	MEP-1	TDEF
	NF-1	TGT3
	NF-GMb	TII
	N-Oct-3	UBP-1
	Oct	WT-1
10	PEA3	Pit-1a
	PPAR	
	PR	
	PU.1	
	PuF	
15	Sp1	
	SRY	
	TCF-1A	
	TFIIB	
	TFIIE	
20	TFIIF	
	TMF	
	YY1	
	Zeste	

25

30

The human GLC1A gene has been placed on the chromosome 1 physical map between four flanking genes (SELL, SELE, GLC1A, APT1LG1, AT3). The mouse homologs of these flanking genes are present in the same order on the mouse chromosome 1, suggesting that the mouse GLC1A gene is located in this syntenic region between the mouse homologues of SELE and APT1LG1.

The expression of human GLC1A was examined by Northern blot analysis of RNA from adult tissues. High levels of expression of the 2.3kb mRNA was found in a wide range of tissues including: heart, skeletal muscle, stomach, thyroid, trachea, bone marrow, thymus, prostate, small intestine and colon. Less abundant

GLC1A expression was observed in lung, pancreas, testis, ovary, spinal cord, lymph node and adrenal gland. GLC1A transcripts were not detected in brain, placenta, liver, kidney, spleen or leukocytes. A similar expression pattern was observed in the mouse. To test the possibility that certain regions of the brain were under represented in poly-A selected mRNA of total brain tissue, a Northern blot prepared with RNA from several
5 different regions of the brain were hybridized using a GLC1A probe. Hybridization was observed in the spinal cord, but not in the cerebellum, cerebral cortex, medulla, occipital lobe, frontal lobe, temporal lobe, or putamen.

Figure 2 illustrates protein motifs that are present in both human and
10 mouse GLC1A proteins. Both the GLC1A nucleic acid sequence and encoded myocilin amino acid sequence show homology to nonmuscle myosin in the N-terminal region and to olfactomedin in the C-terminal region. In addition, both human and mouse GLC1A proteins contain a leucine zipper domain similar to that seen in kinectin and other
15 cytoskeletal proteins in the myosin-like domain (spanning amino acids 71-152). This motif consists of two subregions spanning amino acids 71-85 and 103-152 in which leucine residues appear three to eight times at every seventh position. Both the human and the mouse GLC1A nucleic acids include 10 putative phosphorylation sites and 4 putative glycosylation sites. In addition to these functional domains, a hydrophobic domain appears at the N-terminus of the myocilin protein and includes a sequence
20 resembling a signal peptide in which the alanine residue at position 18 may be a possible cleavage site.

Further analysis reveals a hydrophobic region between amino acids 17-37 and 426-44. However, the length and degree of hydrophobicity of these domains suggests that they are not membrane spanning. The carboxy-terminal three amino acids
25 of human GLC1A protein are serine, lysine and methionine. This sequence has been shown to function as a peroxisome targeting sequence in other proteins (Subramani, S (1993) *Ann. Rev. of Cell Bio.* 9:445-478). However, no such putative targeting sequence is present in the mouse protein. Western blot analysis of human GLC1A protein reveals bands at 57 and 59 kD, confirming the predicted protein size and providing evidence that
30 the protein may be glycosylated. These findings suggest that myocilin is a novel cytoskeletal protein involved in the development of neuroepithelium, such as photoreceptor cells.

Figure 3 shows an alignment of the predicted amino acid sequence for the mouse and human GLC1A genes and indicates the position of sixteen mutations with

respect to the mouse and human GLC1A protein sequences. Fourteen of these mutations are missense mutations that result in single amino acid substitutions. Twelve of these occur at amino acids that are conserved between human and mouse while two occur at amino acids that are not conserved. The two remaining mutations include an insertion that disrupts two conserved amino acids and a nonsense mutation that results in the truncation of the terminal 136 amino acids of the GLC1A protein and the loss of 121 conserved residues. Thus, the percentage of disease causing mutations found in amino acids conserved between mouse and human (88%) is not significantly different from the overall protein conservation across species (82%).

Importantly, the GLC1A nucleic acid sequence differs substantially from the TIGR gene sequence reported in International Patent Application No. WO 96/14411 (GenBank accession nos. R95491, R95447, R95443 and R947209). In fact, as reported, the TIGR gene sequence does not encode a functional protein.

A summary of the differences between the GLC1A gene disclosed herein, and the TIGR gene are presented in Table 5.

Table 5
Differences Between GLC1A and TIGR Gene Sequences

1. The "C" at bp #331 of the GLC1A DNA coding sequence is not present in the TIGR sequence.
2. The 29 bps "AGGGGCTGCAGAGGGAGCTGGGCACCCTG" (SEQ ID NO. 11) at bp #344-372 of the GLC1A DNA coding sequence are not included in the TIGR sequence.

Errors 1 and 2 cause the TIGR sequence to wrongly predict 4 amino acids and exclude 10 amino acids from the protein sequence.

3. The "C" at bp #559 of the GLC1A DNA coding sequence is not present in the TIGR sequence.

4. A "T" is wrongly inserted between bp #560 and #561 of the GLC1A DNA coding sequence in the TIGR sequence.

5

Errors 3 and 4 cause the TIGR sequence to incorrectly predict a serine amino acid at residue #187 instead of a glutamine.

10

5. The 9 bps "CTCAGGAGT" present at bps 706-714 of the GLC1A DNA coding sequence are wrongly duplicated and inserted between bp 714 and 715 in the TIGR sequence.

15

6. Consequently, the TIGR DNA sequence incorrectly predicts that 3 amino acids are inserted into the GLC1A protein sequence.

20

6. A "T" is incorrectly inserted between bp #841 and #842 of the GLC1A DNA coding sequence in the TIGR sequence.

7. The "G" at bp #891 of the GLC1A DNA coding sequence is not present in the TIGR sequence.

25

Errors 6 and 7 cause 17 amino acids predicted by the GLC1A DNA coding sequence to be out of frame in the TIGR sequence.

30

8. A "G" at bp #979 of the GLC1A DNA coding sequence is replaced with a "C" in the TIGR sequence.
9. A "C" at bp #980 of the GLC1A DNA coding sequence is replaced with a "G" in the TIGR sequence.

Errors 8. and 9. cause the TIGR sequence to wrongly predict an arginine amino acid at residue #327 instead of an alanine.

5

The above 9 errors in the TIGR GLC1A sequence result in 45 nucleotide differences that cause 42 incorrect amino acid predictions. Therefore the human TIGR amino acid sequence is only about 91.67% identical to the human myocilin protein sequence and the human TIGR gene sequence is only about 97% identical to the human GLC1A sequence.

10.

The identification of this disease gene increases the understanding of the pathophysiology of glaucoma, which in turn facilitates the development of assays for identifying molecules that modulate (e.g. agonize or antagonize) the bioactivity of a functional or mutant TIGR gene or protein. A therapeutically effective amount of these molecules can be administered to a subject with glaucoma or at risk for developing glaucoma to prevent or reduce the severity of the condition.

15

In addition, the establishment of the disease-causing nature of each GLC1A sequence variant and the associated penetrance and age of onset, as set forth herein, enables a clinician to provide patients, who harbor a particular sequence change, with useful information regarding their risk of developing glaucoma.

20

4.2 Definitions

For convenience, the meaning of certain terms and phrases employed in the specification, examples, and appended claims are provided below.

25

The term "agonist", as used herein, is meant to refer to an agent (e.g., a myocilin therapeutic) that directly or indirectly enhances, supplements or potentiates a wildtype or mutant myocilin bioactivity.

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The term "antagonist", as used herein, is meant to refer to an agent (e.g. a myocilin therapeutic) that directly or indirectly prevents, minimizes or suppresses a wildtype or mutant myocilin bioactivity.

"Cells", "host cells" or "recombinant host cells" are terms used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or

environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A "chimeric protein" or "fusion protein" is a fusion of a first amino acid sequence encoding one of the subject polypeptides with a second amino acid sequence defining a domain (e.g. polypeptide portion) foreign to and not substantially homologous with any domain of one of the proteins. A chimeric protein may present a foreign domain which is found (albeit in a different protein) in an organism which also expresses the first protein, or it may be an "interspecies", "intergenic", etc. fusion of protein structures expressed by different kinds of organisms. In general, a fusion protein can be represented by the general formula X-myocilin-Y, wherein myocilin represents at least a portion of the protein which is derived from one of the myocilin proteins, and X and Y are independently absent or represent amino acid sequences which are not related to one of the myocilin sequences in an organism, including naturally occurring mutants.

"Complementary" sequences as used herein refer to sequences which have sufficient complementarity to be able to hybridize, forming a stable duplex.

A "delivery complex" shall mean a targeting means (e.g. a molecule that results in higher affinity binding of a gene, protein, polypeptide or peptide to a target cell surface and/or increased cellular uptake by a target cell). Examples of targeting means include: sterols (e.g. cholesterol), lipids (e.g. a cationic lipid, virosome or liposome), viruses (e.g. adenovirus, adeno-associated virus, and retrovirus) or target cell specific binding agents (e.g. ligands recognized by target cell specific receptors). Preferred complexes are sufficiently stable *in vivo* to prevent significant uncoupling prior to internalization by the target cell. However, the complex is cleavable under appropriate conditions within the cell so that the gene, protein, polypeptide or peptide is released in a functional form.

As is well known, genes for a particular polypeptide may exist in single or multiple copies within the genome of an individual. Such duplicate genes may be identical or may have certain modifications, including nucleotide substitutions, additions or deletions, which all still code for polypeptides having substantially the same activity. The term "DNA sequence encoding a myocilin polypeptide" may thus refer to one or more genes within a particular individual. Moreover, certain differences in nucleotide sequences may exist between individual organisms, which are called alleles. Such allelic differences may or may not result in differences in amino acid sequence of the encoded polypeptide yet still encode a protein with the same biological activity.

As used herein, the term "gene" or "recombinant gene" refers to a nucleic acid molecule comprising an open reading frame encoding one of the polypeptides of the present invention, including both exon and (optionally) intron sequences. A "recombinant gene" refers to nucleic acid encoding a myocilin polypeptide and comprising GLC1A-encoding exon sequences, though it may optionally include intron sequences which are either derived from a chromosomal GLC1A gene or from an unrelated chromosomal gene. Exemplary recombinant genes encoding the subject myocilin polypeptides are represented in SEQ ID NO 7 and 9. The term "intron" refers to a DNA sequence present in a given GLC1A gene which is not translated into protein and is generally found between exons.

"Homology" or "identity" or "similarity" refers to sequence similarity between two peptides or between two nucleic acid molecules. Homology can be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same base or amino acid, then the molecules are homologous at that position. A degree of homology between sequences is a function of the number of matching or homologous positions shared by the sequences. An "unrelated" or "non-homologous" sequence shares less than 40 % identity, though preferably less than 25 % identity, with one of the GLC1A sequences of the present invention.

The term "interact" as used herein is meant to include detectable interactions between molecules, such as can be detected using, for example, a yeast two hybrid assay. The term interact is also meant to include "binding" interactions between molecules. Interactions may, for example, be protein-protein or protein-nucleic acid in nature.

The term "isolated" as used herein with respect to nucleic acids, such as DNA or RNA, refers to molecules separated from other DNAs, or RNAs, respectively, that are present in the natural source of the macromolecule. For example, an isolated nucleic acid encoding one of the subject GLC1A polypeptides preferably includes no more than 10 kilobases (kb) of nucleic acid sequence which naturally immediately flanks the GLC1A gene in genomic DNA, more preferably no more than 5kb of such naturally occurring flanking sequences, and most preferably less than 1.5kb of such naturally occurring flanking sequence. The term isolated as used herein also refers to a nucleic acid or peptide that is substantially free of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or

other chemicals when chemically synthesized. Moreover, an "isolated nucleic acid" is meant to include nucleic acid fragments which are not naturally occurring as fragments and would not be found in the natural state. The term "isolated" is also used herein to refer to polypeptides which are isolated from other cellular proteins and is meant to encompass both purified and recombinant polypeptides.

The term "modulation" as used herein refers to both upregulation, (i.e., activation or stimulation), for example by agonizing; and downregulation, (i.e. inhibition or suppression) for example by antagonizing a myocilin bioactivity.

A "myocilin bioactivity", "biological activity" or "activity" is meant to refer to a cytoskeletal or antigenic function that is directly or indirectly preformed by a myocilin polypeptide (whether in its native or denatured conformation), or by any subsequence thereof. Cytoskeletal functions include processes involved with the development or structure of ciliated neuroepithelium (e.g. comprising photoreceptor cells). Antigenic functions include possession of an epitope or antigenic site that is capable of cross-reacting with antibodies raised against a naturally occurring or denatured myocilin polypeptide or fragment thereof.

The "non-human animals" of the invention include mammals such as rodents, non-human primates, sheep, dog, cow, chickens, amphibians, reptiles, etc. Preferred non-human animals are selected from the rodent family including rat and mouse, most preferably mouse, though transgenic amphibians, such as members of the *Xenopus* genus, and transgenic chickens can also provide important tools for understanding and identifying agents which can affect, for example, embryogenesis and tissue formation. The term "chimeric animal" is used herein to refer to animals in which the recombinant gene is found, or in which the recombinant gene is expressed in some but not all cells of the animal. The term "tissue-specific chimeric animal" indicates that one of the recombinant GLC1A genes is present and/or expressed or disrupted in some tissues but not others.

As used herein, the term "nucleic acid" refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term should also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs, and, as applicable to the embodiment being described, single (sense or antisense) and double-stranded polynucleotides.

As used herein, the term "promoter" means a DNA sequence that regulates expression of a selected DNA sequence operably linked to the promoter, and

which effects expression of the selected DNA sequence in cells. The term encompasses "tissue specific" promoters, i.e. promoters, which effect expression of the selected DNA sequence only in specific cells (e.g. cells of a specific tissue). The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well. The term also encompasses non-tissue specific promoters and promoters that constitutively express or that are inducible (i.e. expression levels can be controlled).

The terms "protein", "polypeptide" and "peptide" are used interchangeably herein when referring to a gene product.

The term "recombinant protein" refers to a polypeptide of the present invention which is produced by recombinant DNA techniques, wherein generally, DNA encoding a myocilin polypeptide is inserted into a suitable expression vector which is in turn used to transform a host cell to produce the heterologous protein. Moreover, the phrase "derived from", with respect to a recombinant GLC1A gene, is meant to include within the meaning of "recombinant protein" those proteins having an amino acid sequence of a native myocilin protein, or an amino acid sequence similar thereto which is generated by mutations including substitutions and deletions (including truncation) of a naturally occurring form of the protein.

"Small molecule" as used herein, is meant to refer to a composition, which has a molecular weight of less than about 5kD and most preferably less than about 4kD. Small molecules can be nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic carbon containing or inorganic molecules. Extensive libraries of chemical or biological (e.g., fungal, bacterial or algal extracts) mixtures are available for screening with the assays of the invention.

As used herein, the term "specifically hybridizes" or "specifically detects" refers to the ability of a nucleic acid molecule of the invention to hybridize to at least approximately 6, 12, 20, 30, 50, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1460, 1470, 1480, 1490 consecutive nucleotides of a vertebrate, preferably GLC1A gene, such as a GLC1A sequence designated in one of SEQ ID Nos: 7 or 9, or a sequence complementary thereto, or naturally occurring mutants thereof, such that it shows at least 10 times more hybridization, preferably at least 50 times more hybridization, and even more preferably at least 100 times more hybridization than it

does to a cellular nucleic acid (e.g., mRNA or genomic DNA) encoding a protein other than a vertebrate GLC1A protein as defined herein.

“Transcriptional regulatory sequence” is a generic term used throughout the specification to refer to DNA sequences, such as initiation signals, enhancers, and promoters, which induce or control transcription of protein coding sequences with which they are operably linked. In preferred embodiments, transcription of one of the recombinant GLC1A genes is under the control of a promoter sequence (or other transcriptional regulatory sequence) which controls the expression of the recombinant gene in a cell-type in which expression is intended. It will also be understood that the recombinant gene can be under the control of transcriptional regulatory sequences which are the same or which are different from those sequences which control transcription of the naturally-occurring forms of myocilin proteins.

As used herein, the term “transfection” means the introduction of a nucleic acid, e.g., an expression vector, into a recipient cell by nucleic acid-mediated gene transfer. “Transformation”, as used herein, refers to a process in which a cell's genotype is changed as a result of the cellular uptake of exogenous DNA or RNA, and, for example, the transformed cell expresses a recombinant form of a mammalian myocilin polypeptide or, in the case of anti-sense expression from the transferred gene, the expression of a naturally-occurring form of the myocilin protein is disrupted.

As used herein, the term “transgene” means a nucleic acid sequence (encoding, e.g., one of the mammalian myocilin polypeptides, or pending an antisense transcript thereto), which is partly or entirely heterologous, i.e., foreign, to the transgenic animal or cell into which it is introduced, or, is homologous to an endogenous gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or is inserted, into the animal's genome in such a way as to alter the genome of the cell into which it is inserted (e.g., it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). A transgene can include one or more transcriptional regulatory sequences and any other nucleic acid, such as introns, that may be necessary for optimal expression of a selected nucleic acid.

A “transgenic animal” refers to any animal, preferably a non-human mammal, bird or an amphibian, in which one or more of the cells of the animal contain heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate

genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or *in vitro* fertilization, but rather is directed to the introduction of a recombinant DNA molecule. This molecule may be integrated within a chromosome, or it may be
5 extrachromosomally replicating DNA. In the typical transgenic animals described herein, the transgene causes cells to express a recombinant form of one of the GLC1A proteins, e.g. either agonistic or antagonistic forms. However, transgenic animals in which the recombinant GLC1A gene is silent are also contemplated, as for example, the FLP or CRE recombinase dependent constructs described below. Moreover, "transgenic
10 animal" also includes those recombinant animals in which gene disruption of one or more GLC1A genes is caused by human intervention, including both recombination and antisense techniques.

The term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of preferred
15 vector is an episome, i.e., a nucleic acid capable of extra-chromosomal replication. Preferred vectors are those capable of autonomous replication and/or expression of nucleic acids to which they are linked. Vectors capable of directing the expression of genes to which they are operatively linked are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the
20 form of "plasmids" which refer generally to circular double stranded DNA loops which, in their vector form are not bound to the chromosome. In the present specification, "plasmid" and "vector" are used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors which serve equivalent functions and which become known in the art
25 subsequently hereto.

4.3 Nucleic Acids of the Present Invention

As described below, one aspect of the invention pertains to isolated nucleic acids comprising nucleotide sequences encoding myocilin polypeptides, and/or
30 equivalents of such nucleic acids. The term equivalent is understood to include nucleotide sequences encoding functionally equivalent myocilin polypeptides or functionally equivalent peptides having an activity of a vertebrate myocilin protein such as described herein. Equivalent nucleotide sequences will include sequences that differ by one or more nucleotide substitutions, additions or deletions, such as allelic variants;

and will, therefore, include sequences that differ from the nucleotide sequence of the GLC1A gene shown in SEQ ID Nos: 7 or 9 due to the degeneracy of the genetic code.

Preferred nucleic acids are vertebrate GLC1A nucleic acids. Particularly preferred vertebrate GLC1A nucleic acids are mammalian. Regardless of species, particularly preferred GLC1A nucleic acids encode polypeptides that are at least 90% similar to an amino acid sequence of human GLC1A. Preferred nucleic acids encode a GLC1A polypeptide comprising an amino acid sequence at least 90% homologous and more preferably 94% homologous with an amino acid sequence of a vertebrate GLC1A, e.g., such as a sequence shown in one of SEQ ID Nos: 8 or 10. Nucleic acids which encode polypeptides at least about 95%, and even more preferably at least about 98-99% similarity with an amino acid sequence represented in SEQ ID Nos.: 8 or 10 are also within the scope of the invention. In a particularly preferred embodiment, the nucleic acid of the present invention encodes an amino acid GLC1A sequence shown in one of SEQ ID No: 8 or 10. In one embodiment, the nucleic acid is a cDNA encoding a peptide having at least one bioactivity of the subject GLC1A polypeptide. Preferably, the nucleic acid includes all or a portion of the nucleotide sequence corresponding to the coding region of SEQ ID Nos: 1-7 or 9.

Still other preferred nucleic acids of the present invention encode a GLC1A polypeptide which includes a polypeptide sequence corresponding to all or a portion of amino acid residues of SEQ ID Nos: 8 or 10, e.g., at least 2, 5, 10, 25, 50, 100, 150 or 200 amino acid residues of that region. For example, preferred nucleic acid molecules for use as probes/primer or antisense molecules (i.e. noncoding nucleic acid molecules) can comprise at least about 6, 12, 20, 30, 50, 100, 125, 150 or 200 base pairs in length, whereas coding nucleic acid molecules can comprise about 200, 250, 300, 350, 400, 410, 420, 430, 435 or 440 base pairs.

Another aspect of the invention provides a nucleic acid which hybridizes to a nucleic acid represented by one of SEQ ID Nos: 1-7 or 9. Appropriate stringency conditions which promote DNA hybridization, for example, 6.0 x sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 x SSC at 50°C, are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 x SSC at 50°C to a high stringency of about 0.2 x SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature,

about 22°C, to high stringency conditions at about 65°C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed. In a preferred embodiment, a GLC1A nucleic acid of the present invention will bind to one of SEQ ID Nos 1 or 2 under moderately stringent
5 conditions, for example at about 2.0 x SSC and about 40°C. In a particularly preferred embodiment, a GLC1A nucleic acid of the present invention will bind to one of SEQ ID Nos: 1-7 or 9 under high stringency conditions.

Preferred nucleic acids have a sequence at least about 75% homologous and more preferably 80% and even more preferably at least about 85% homologous with
10 an amino acid sequence of a mammalian GLC1A, e.g., such as a sequence shown in one of SEQ ID Nos: 8 and 10. Nucleic acids at least about 90%, more preferably about 95%, and most preferably at least about 98-99% homologous with a nucleic sequence represented in one of SEQ ID Nos: 8 and 10 are of course also within the scope of the invention. In preferred embodiments, the nucleic acid is a mammalian GLC1A gene and
15 in particularly preferred embodiments, includes all or a portion of the nucleotide sequence corresponding to the coding region of one of SEQ ID Nos: 1-7 or 9.

Nucleic acids having a sequence that differs from the nucleotide sequences shown in one of SEQ ID Nos: 1-7 or 9 due to degeneracy in the genetic code are also within the scope of the invention. Such nucleic acids encode functionally
20 equivalent peptides (i.e., a peptide having a biological activity of a myocilin polypeptide) but differ in sequence from the sequence shown in the sequence listing due to degeneracy in the genetic code. For example, a number of amino acids are designated by more than one triplet. Codons that specify the same amino acid, or synonyms (for example, CAU and CAC each encode histidine) may result in "silent" mutations which
25 do not affect the amino acid sequence of a myocilin polypeptide. However, it is expected that DNA sequence polymorphisms that do lead to changes in the amino acid sequences of the subject myocilin polypeptides will exist among mammals. One skilled in the art will appreciate that these variations in one or more nucleotides (e.g., up to about 3-5% of the nucleotides) of the nucleic acids encoding polypeptides having an
30 activity of a mammalian myocilin polypeptide may exist among individuals of a given species due to natural allelic variation.

As indicated by the examples set out below, myocilin protein-encoding nucleic acids can be obtained from mRNA present in any of a number of eukaryotic cells. It should also be possible to obtain nucleic acids encoding mammalian myocilin

polypeptides of the present invention from genomic DNA from both adults and embryos. For example, a gene encoding a myocilin protein can be cloned from either a cDNA or a genomic library in accordance with protocols described herein, as well as those generally known to persons skilled in the art. Examples of tissues and/or libraries suitable for isolation of the subject nucleic acids include photoreceptor cells of the retina, among others. A cDNA encoding a myocilin protein can be obtained by isolating total mRNA from a cell, e.g. a vertebrate cell, a mammalian cell, or a human cell, including embryonic cells. Double stranded cDNAs can then be prepared from the total mRNA, and subsequently inserted into a suitable plasmid or bacteriophage vector using any one of a number of known techniques. The gene encoding a mammalian myocilin protein can also be cloned using established polymerase chain reaction techniques in accordance with the nucleotide sequence information provided by the invention. The nucleic acid of the invention can be DNA or RNA. A preferred nucleic acid is a cDNA represented by a sequence selected from the group consisting of SEQ ID Nos:1 and 2.

4.3.1. Vectors.

This invention also provides expression vectors containing a nucleic acid encoding a myocilin polypeptide, operably linked to at least one transcriptional regulatory sequence. "Operably linked" is intended to mean that the nucleotide sequence is linked to a regulatory sequence in a manner which allows expression of the nucleotide sequence. Regulatory sequences are art-recognized and are selected to direct expression of the subject mammalian myocilin proteins. Accordingly, the term "transcriptional regulatory sequence" includes promoters, enhancers and other expression control elements. Such regulatory sequences are described in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). In one embodiment, the expression vector includes a recombinant gene encoding a peptide having an agonistic activity of a subject myocilin polypeptide, or alternatively, encoding a peptide which is an antagonistic form of the myocilin protein. Such expression vectors can be used to transfect cells and thereby produce polypeptides, including fusion proteins, encoded by nucleic acids as described herein. Moreover, the gene constructs of the present invention can also be used as a part of a gene therapy protocol to deliver nucleic acids encoding either an agonistic or antagonistic form of one of the subject myocilin proteins. Thus, another aspect of the invention features expression vectors for *in vivo* or *in vitro* transfection and expression of a myocilin

polypeptide in particular cell types so as to reconstitute the function of, or alternatively, abrogate the function of myocilin-induced signaling in a tissue. This could be desirable, for example, when the naturally-occurring form of the protein is misexpressed; or to deliver a form of the protein which alters differentiation of tissue. Expression vectors
5 may also be employed to inhibit neoplastic transformation.

In addition to viral transfer methods, such as those illustrated above, non-viral methods can also be employed to cause expression of a subject myocilin polypeptide in the tissue of an animal. Most nonviral methods of gene transfer rely on normal mechanisms used by mammalian cells for the uptake and intracellular transport
10 of macromolecules. In preferred embodiments, non-viral targeting means of the present invention rely on endocytic pathways for the uptake of the subject myocilin polypeptide gene by the targeted cell. Exemplary targeting means of this type include liposomal derived systems, poly-lysine conjugates, and artificial viral envelopes.

15 4.3.2. Probes and Primers

Moreover, the nucleotide sequences determined from the cloning of GLC1A genes from mammalian organisms will further allow for the generation of probes and primers designed for use in identifying and/or cloning homologs in other cell types, e.g. from other tissues, as well as homologs from other mammalian organisms.

20 For instance, the present invention also provides a probe/primer comprising a substantially purified oligonucleotide, which oligonucleotide comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least approximately 12, preferably 25, more preferably 40, 50 or 75 consecutive nucleotides of sense or anti-sense sequence selected from the group consisting of SEQ ID Nos: 1-7 or 9, or naturally
25 occurring mutants thereof. For instance, primers based on the nucleic acid represented in SEQ ID Nos: 1-7 or 9 can be used in PCR reactions to clone homologs. Preferred primer pairs of the invention are set forth as SEQ ID Nos. 12 and 13; 14 and 15; 16 and 17; 18 and 19; 20 and 21; 22 and 23; 24 and 25; 26 and 27; 28 and 29; 30 and 31; 32 and 33; 34 and 35; 36 and 37; 38 and 39; 40 and 41; 42 and 43; 44 and 45; and 46 and 47.

30 Likewise, probes based on the subject GLC1A sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto and able to be detected, e.g. the label group can be selected from amongst radioisotopes, fluorescent compounds, enzymes, and enzyme co-factors, etc.

As discussed in more detail below, such probes can also be used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a myocilin protein, such as by measuring a level of a myocilin -encoding nucleic acid in a sample of cells from a patient; e.g. detecting GLC1A mRNA levels or determining whether a genomic GLC1A gene has been mutated or deleted. Briefly, nucleotide probes can be generated from the subject GLC1A genes which facilitate histological screening of intact tissue and tissue samples for the presence (or absence) of myocilin-encoding transcripts. Similar to the diagnostic uses of anti-myocilin antibodies, the use of probes directed to GLC1A messages, or to genomic GLC1A sequences, can be used for both predictive and therapeutic evaluation of subjects. Used in conjunction with immunoassays as described herein, the oligonucleotide probes can help facilitate the determination of the molecular basis for a developmental disorder which may involve some abnormality associated with expression (or lack thereof) of a myocilin protein. For instance, variation in polypeptide synthesis can be differentiated from a mutation in a coding sequence.

4.3.3. Antisense, Ribozyme and Triplex Techniques

One aspect of the invention relates to the use of the isolated nucleic acid in "antisense" therapy. As used herein, "antisense" therapy refers to administration or *in situ* generation of oligonucleotide molecules or their derivatives which specifically hybridize (e.g. bind) under cellular conditions, with the cellular mRNA and/or genomic DNA encoding one or more of the subject GLC1A proteins so as to inhibit expression of that protein, e.g. by inhibiting transcription and/or translation. The binding may be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interactions in the major groove of the double helix. In general, "antisense" therapy refers to the range of techniques generally employed in the art, and includes any therapy which relies on specific binding to oligonucleotide sequences.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid which, when transcribed in the cell, produces RNA which is complementary to at least a unique portion of the cellular mRNA which encodes a myocilin protein. Alternatively, the antisense construct is an oligonucleotide probe which is generated *ex vivo* and which, when introduced into the cell causes inhibition of expression by hybridizing with the mRNA and/or genomic sequences of a GLC1A gene. Such oligonucleotide probes are preferably modified oligonucleotides

which are resistant to endogenous nucleases, e.g. exonucleases and/or endonucleases, and are therefore stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Patents 5,176,996; 5,264,564; and 5,256,775). Additionally,
5 general approaches to constructing oligomers useful in antisense therapy have been reviewed, for example, by Van der Krol et al. (1988) *Biotechniques* 6:958-976; and Stein et al. (1988) *Cancer Res* 48:2659-2668. With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site, e.g., between the -
10 and +10 regions of the GLC1A nucleotide sequence of interest, are preferred.

10 Antisense approaches involve the design of oligonucleotides (either DNA or RNA) that are complementary to GLC1A mRNA. The antisense oligonucleotides will bind to the GLC1A mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, means a sequence having sufficient
15 complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an
20 RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Oligonucleotides that are complementary to the 5' end of the message, e.g., the 5' untranslated sequence up to and including the AUG initiation codon, should
25 work most efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated sequences of mRNAs have recently been shown to be effective at inhibiting translation of mRNAs as well. (Wagner, R. 1994. *Nature* 372:333). Therefore, oligonucleotides complementary to either the 5' or 3' untranslated, non-coding regions of a GLC1A gene could be used in an antisense approach to inhibit
30 translation of endogenous GLC1A mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are less efficient inhibitors of translation but could be used in accordance with the invention. Whether designed to hybridize to the 5', 3' or coding region of GLC1A mRNA, antisense

nucleic acids should be at least six nucleotides in length, and are preferably oligonucleotides ranging from 6 to about 50 nucleotides in length. In certain embodiments, the oligonucleotide is at least 10 nucleotides, at least 17 nucleotides, at least 25 nucleotides, or at least 50 nucleotides.

5 Regardless of the choice of target sequence, it is preferred that *in vitro* studies are first performed to quantitate the ability of the antisense oligonucleotide to quantitate the ability of the antisense oligonucleotide to inhibit gene expression. It is preferred that these studies utilize controls that distinguish between antisense gene inhibition and nonspecific biological effects of oligonucleotides. It is also preferred that
10 these studies compare levels of the target RNA or protein with that of an internal control RNA or protein. Additionally, it is envisioned that results obtained using the antisense oligonucleotide are compared with those obtained using a control oligonucleotide. It is preferred that the control oligonucleotide is of approximately the same length as the test oligonucleotide and that the nucleotide sequence of the oligonucleotide differs from the
15 antisense sequence no more than is necessary to prevent specific hybridization to the target sequence.

 The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate
20 backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre et al., 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. WO 88/09810,
25 published December 15, 1988) or the blood-brain barrier (see, e.g., PCT Publication No. WO 89/10134, published April 25, 1988), hybridization-triggered cleavage agents. (See, e.g., Krol et al., 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport
30 agent, hybridization-triggered cleavage agent, etc.

 The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine,

5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, 5
beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and
10 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including but not limited to arabinose, 2-fluoroarabinose, xylulose, and hexose.

15 In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

20 In yet another embodiment, the antisense oligonucleotide is an α -anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual conformation, the strands run parallel to each other (Gautier et al., 1987, *Nucl. Acids Res.* 15:6625-6641). The oligonucleotide is a 2'-O-methylribonucleotide (Inoue et al., 1987, *Nucl. Acids Res.* 15:6131-6148), or a chimeric RNA-DNA analogue (Inoue et al.,
25 1987, *FEBS Lett.* 215:327-330).

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g. by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al.
30 (1988, *Nucl. Acids Res.* 16:3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85:7448-7451), etc.

While antisense nucleotides complementary to the GLC1A coding region sequence could be used, those complementary to the transcribed untranslated region are most preferred.

5 The antisense molecules should be delivered to cells which express the myocilin *in vivo*. A number of methods have been developed for delivering antisense DNA or RNA to cells; *e.g.*, antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systematically.

10 However, it is often difficult to achieve intracellular concentrations of the antisense sufficient to suppress translation of endogenous mRNAs. Therefore a preferred approach utilizes a recombinant DNA construct in which the antisense oligonucleotide is placed under the control of a strong pol III or pol II promoter. The use of such a construct to transfect target cells in the patient will result in the
15 transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous GLC1A transcripts and thereby prevent translation of the GLC1A mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be
20 transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequence encoding the antisense RNA can be by any promoter known in the art to act in mammalian, preferably human cells. Such promoters can be inducible
25 or constitutive. Such promoters include but are not limited to: the SV40 early promoter region (Bernoist and Chambon, 1981, *Nature* 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., 1980, *Cell* 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, *Proc. Natl. Acad. Sci. U.S.A.* 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al, 1982, *Nature* 296:39-42), etc. Any type of plasmid, cosmid, YAC or viral vector can
30 be used to prepare the recombinant DNA construct which can be introduced directly into the tissue site; *e.g.*, the choroid plexus or hypothalamus. Alternatively, viral vectors can be used which selectively infect the desired tissue; (*e.g.*, for brain, herpesvirus vectors

may be used), in which case administration may be accomplished by another route (e.g., systematically).

Ribozyme molecules designed to catalytically cleave GLC1A mRNA transcripts can also be used to prevent translation of GLC1A mRNA and expression of myocilin. (See, e.g., PCT International Publication WO 90/11364, published October 4, 1990; Sarver et al., 1990, *Science* 247:1222-1225). While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy GLC1A mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, 1988, *Nature*, 334:585-591. There are hundreds of potential hammerhead ribozyme cleavage sites within the nucleotide sequence of human GLC1A cDNA. Preferably the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the GLC1A mRNA; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

The ribozymes of the present invention also include RNA endoribonucleases (hereinafter "Cech-type ribozymes") such as the one which occurs naturally in *Tetrahymena Thermophila* (known as the IVS, or L-19 IVS RNA) and which has been extensively described by Thomas Cech and collaborators (Zaug, et al., 1984, *Science*, 224:574-578; Zaug and Cech, 1986, *Science*, 231:470-475; Zaug, et al., 1986, *Nature*, 324:429-433; published International patent application No. WO 88/04300 by University Patents Inc.; Been and Cech, 1986, *Cell*, 47:207-216). The Cech-type ribozymes have an eight base pair active site which hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. The invention encompasses those Cech-type ribozymes which target eight base-pair active site sequences that are present in GLC1A.

As in the antisense approach, the ribozymes can be composed of modified oligonucleotides (e.g. for improved stability, targeting, etc.) and should be delivered to cells which express the GLC1A *in vivo* e.g., hypothalamus and/or the choroid plexus. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to

destroy endogenous GLC1A messages and inhibit translation. Because ribozymes unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Endogenous GLC1A gene expression can also be reduced by inactivating or "knocking out" the GLC1A gene or its promoter using targeted homologous recombination. (e.g, see Smithies et al., 1985, *Nature* 317:230-234; Thomas & Capecchi, 1987, *Cell* 51:503-512; Thompson et al., 1989 *Cell* 5:313-321; each of which is incorporated by reference herein in its entirety). For example, a mutant, non-functional GLC1A (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous GLC1A gene (either the coding regions or regulatory regions of the GLC1A gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express GLC1A *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the GLC1A gene. Such approaches are particularly suited in the agricultural field where modifications to ES (embryonic stem) cells can be used to generate animal offspring with an inactive GLC1A (e.g., see Thomas & Capecchi 1987 and Thompson 1989, *supra*). However this approach can be adapted for use in humans provided the recombinant DNA constructs are directly administered or targeted to the required site *in vivo* using appropriate viral vectors, e.g., herpes virus vectors for delivery to brain tissue; e.g., the hypothalamus and/or choroid plexus.

Alternatively, endogenous GLC1A gene expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of the GLC1A gene (i.e., the GLC1A promoter and/or enhancers) to form triple helical structures that prevent transcription of the GLC1A gene in target cells in the body. (See generally, Helene, C. 1991, *Anticancer Drug Des.*, 6(6):569-84; Helene, C., et al., 1992, *Ann. N.Y. Acad. Sci.*, 660:27-36; and Maher, L.J., 1992, *Bioassays* 14(12):807-15).

Likewise, the antisense constructs of the present invention, by antagonizing the normal biological activity of one of the myocilin proteins, can be used in the manipulation of tissue, e.g. tissue differentiation, both *in vivo* and for *ex vivo* tissue cultures.

Furthermore, the anti-sense techniques (e.g. microinjection of antisense molecules, or transfection with plasmids whose transcripts are antisense with regard to a GLC1A mRNA or gene sequence) can be used to investigate role of myocilin in developmental events, as well as the normal cellular function of myocilin in adult tissue.

Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals, as detailed below.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA, followed by an endonucleolytic cleavage. The composition of ribozyme molecules must include one or more sequences complementary to the target gene mRNA, and must include the well known catalytic sequence responsible for mRNA cleavage. For this sequence, see U.S. Pat. No. 5,093,246, which is incorporated by reference herein in its entirety. As such within the scope of the invention are engineered hammerhead motif ribozyme molecules that specifically and efficiently catalyze endonucleolytic cleavage of RNA sequences encoding myocilin proteins.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the molecule of interest for ribozyme cleavage sites which include the following sequences, GUA, GUU and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides corresponding to the region of the target gene containing the cleavage site may be evaluated for predicted structural features, such as secondary structure, that may render the oligonucleotide sequence unsuitable. The suitability of candidate sequences may also be evaluated by testing their accessibility to hybridization with complementary oligonucleotides, using ribonuclease protection assays.

Nucleic acid molecules to be used in triple helix formation for the inhibition of transcription are preferably single stranded and composed of deoxyribonucleotides. The base composition of these oligonucleotides should promote triple helix formation via Hoogsteen base pairing rules, which generally require sizable stretches of either purines or pyrimidines to be present on one strand of a duplex. Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine-rich, for example, containing a stretch of G residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in CGC triplets across the three strands in the triplex.

Alternatively, the potential sequences that can be targeted for triple helix formation may be increased by creating a so called "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizable stretch of either purines or pyrimidines to be present on one strand of a duplex.

Antisense RNA and DNA, ribozyme, and triple helix molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

Moreover, various well-known modifications to nucleic acid molecules may be introduced as a means of increasing intracellular stability and half-life. Possible modifications include but are not limited to the addition of flanking sequences of ribonucleotides or deoxyribonucleotides to the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the oligodeoxyribonucleotide backbone.

4.4. Polypeptides of the Present Invention

The present invention also makes available myocilin polypeptides, which are isolated from, or otherwise substantially free of other cellular proteins, especially other signal transduction factors and/or transcription factors which may normally be associated with the myocilin polypeptide. The term "substantially free of other cellular proteins" (also referred to herein as "contaminating proteins") or "substantially pure or purified preparations" are defined as encompassing preparations of myocilin polypeptides having less than about 20% (by dry weight) contaminating protein, and preferably having less than about 5% contaminating protein. Functional forms of the subject polypeptides can be prepared, for the first time, as purified preparations by using a cloned gene as described herein. By "purified", it is meant, when referring to a peptide or DNA or RNA sequence,

that the indicated molecule is present in the substantial absence of other biological macromolecules, such as other proteins. The term "purified" as used herein preferably means at least 80% by dry weight, more preferably in the range of 95-99% by weight, and most preferably at least 99.8% by weight, of biological macromolecules of the same type present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 5000, can be present). The term "pure" as used herein preferably has the same numerical limits as "purified" immediately above. "Isolated" and "purified" do not encompass either natural materials in their native state or natural materials that have been separated into components (e.g., in an acrylamide gel) but not obtained either as pure (e.g. lacking contaminating proteins, or chromatography reagents such as denaturing agents and polymers, e.g. acrylamide or agarose) substances or solutions. In preferred embodiments, purified GLC1A preparations will lack any contaminating proteins from the same animal from which myocilin is normally produced, as can be accomplished by recombinant expression of, for example, a human myocilin protein in a non-human cell.

Full length proteins or fragments corresponding to one or more particular motifs and/or domains or to arbitrary sizes, for example, at least 5, 10, 25, 50, 75, 100, 125, 150 amino acids in length are within the scope of the present invention.

For example, isolated myocilin polypeptides can include all or a portion of an amino acid sequences corresponding to a myocilin polypeptide represented in SEQ ID Nos: 8 or 10. Isolated peptidyl portions of myocilin proteins can be obtained by screening peptides recombinantly produced from the corresponding fragment of the nucleic acid encoding such peptides. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, a myocilin polypeptide of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or preferably divided into overlapping fragments of a desired length. The fragments can be produced (recombinantly or by chemical synthesis) and tested to identify those peptidyl fragments which can function as either agonists or antagonists of a wild-type (e.g., "authentic") myocilin protein.

Another aspect of the present invention concerns recombinant forms of the myocilin proteins. Recombinant polypeptides preferred by the present invention, in addition to native myocilin proteins, are at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% homologous with an amino acid sequence represented by SEQ ID Nos: 8 or 10. In a preferred embodiment, a myocilin protein of the present invention is a myocilin

protein. In a particularly preferred embodiment, a myocilin protein comprises the coding sequence of one of SEQ ID No.: 1-7, or 9. In particularly preferred embodiments, a myocilin protein has a myocilin bioactivity.

5 The present invention further pertains to recombinant forms of one of the subject myocilin polypeptides which are encoded by genes derived from a mammalian organism, and which have amino acid sequences evolutionarily related to the myocilin proteins represented in SEQ ID Nos: 8 or 10. Such recombinant myocilin polypeptides preferably are capable of functioning in one of either role of an agonist or antagonist of at least one biological activity of a wild-type ("authentic") myocilin protein of the appended
10 sequence listing. The term "evolutionarily related to", with respect to amino acid sequences of myocilin proteins, refers to both polypeptides having amino acid sequences which have arisen naturally, and also to mutational variants of myocilin polypeptides which are derived, for example, by combinatorial mutagenesis. Such evolutionarily derived myocilin polypeptides preferred by the present invention have a myocilin bioactivity and are at least
15 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous with the amino acid sequence selected from the group consisting of SEQ ID Nos: 8 or 10.

In general, polypeptides referred to herein as having an activity of a myocilin protein (e.g., are "bioactive") are defined as polypeptides which include an amino acid sequence corresponding (e.g., identical or homologous) to all or a portion of the amino acid
20 sequences of a myocilin protein shown in SEQ ID Nos: 8 or 10 and which mimic or antagonize all or a portion of the biological/biochemical activities of a naturally occurring myocilin protein. According to the present invention, a polypeptide has biological activity if it is a specific agonist or antagonist of a naturally-occurring form of a myocilin protein.

The present invention further pertains to methods of producing the subject
25 myocilin polypeptides. For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding the subject polypeptides can be cultured under appropriate conditions to allow expression of the peptide to occur. The cells may be harvested, lysed and the protein isolated. A cell culture includes host cells, media and other byproducts. Suitable media for cell culture are well known in the art. The
30 recombinant myocilin polypeptide can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such peptide. In a preferred

embodiment, the recombinant myocilin polypeptide is a fusion protein containing a domain which facilitates its purification, such as GST fusion protein or poly(His) fusion protein.

Moreover, it will be generally appreciated that, under certain circumstances, it may be advantageous to provide homologs of one of the subject myocilin polypeptides which function in a limited capacity as one of either a myocilin agonist (mimetic) or a myocilin antagonist, in order to promote or inhibit only a subset of the biological activities of the naturally-occurring form of the protein. Thus, specific biological effects can be elicited by treatment with a homolog of limited function, and with fewer side effects relative to treatment with agonists or antagonists which are directed to all of the biological activities of naturally occurring forms of myocilin proteins.

Homologs of each of the subject myocilin proteins can be generated by mutagenesis, such as by discrete point mutation(s), or by truncation. For instance, mutation can give rise to homologs which retain substantially the same, or merely a subset, of the biological activity of the myocilin polypeptide from which it was derived. Alternatively, antagonistic forms of the protein can be generated which are able to inhibit the function of the naturally occurring form of the protein, such as by competitively binding to a downstream or upstream member of the biochemical pathway, which includes the myocilin protein. In addition, agonistic forms of the protein may be generated which are constitutively active. Thus, the human myocilin protein and homologs thereof provided by the subject invention may be either positive or negative regulators of gene expression.

The recombinant myocilin polypeptides of the present invention also include homologs of the authentic myocilin proteins, such as versions of those protein which are resistant to proteolytic cleavage, as for example, due to mutations which alter ubiquitination or other enzymatic targeting associated with the protein.

Myocilin polypeptides may also be chemically modified to create derivatives by forming covalent or aggregate conjugates with other chemical moieties, such as glycosyl groups, lipids, phosphate, acetyl groups and the like. Covalent derivatives of myocilin proteins can be prepared by linking the chemical moieties to functional groups on amino acid sidechains of the protein or at the N-terminus or at the C-terminus of the polypeptide.

Modification of the structure of the subject myocilin polypeptides can be for such purposes as enhancing therapeutic or prophylactic efficacy, stability (e.g., *ex vivo* shelf life and resistance to proteolytic degradation *in vivo*), or post-translational modifications (e.g., to alter phosphorylation pattern of protein). Such modified peptides, when designed to retain at least one activity of the naturally-occurring form of the protein, or to produce

specific antagonists thereof, are considered functional equivalents of the myocilin polypeptides described in more detail herein. Such modified peptides can be produced, for instance, by amino acid substitution, deletion, or addition.

For example, it is reasonable to expect that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid (i.e. isosteric and/or isoelectric mutations) will not have a major effect on the biological activity of the resulting molecule. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids are can be divided into four families: (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine, histidine; (3) nonpolar = alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar = glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. In similar fashion, the amino acid repertoire can be grouped as (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine histidine, (3) aliphatic = glycine, alanine, valine, leucine, isoleucine, serine, threonine, with serine and threonine optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic = phenylalanine, tyrosine, tryptophan; (5) amide = asparagine, glutamine; and (6) sulfur - containing = cysteine and methionine. (see, for example, *Biochemistry*, 2nd ed., Ed. by L. Stryer, WH Freeman and Co.: 1981). Whether a change in the amino acid sequence of a peptide results in a functional myocilin homolog (e.g. functional in the sense that the resulting polypeptide mimics or antagonizes the wild-type form) can be readily determined by assessing the ability of the variant peptide to produce a response in cells in a fashion similar to the wild-type protein, or competitively inhibit such a response. Polypeptides in which more than one replacement has taken place can readily be tested in the same manner.

This invention further contemplates a method for generating sets of combinatorial mutants of the subject myocilin proteins as well as truncation mutants, and is especially useful for identifying potential variant sequences (e.g. homologs) that are functional in modulating gene expression. The purpose of screening such combinatorial libraries is to generate, for example, novel myocilin homologs which can act as either agonists or antagonist, or alternatively, possess novel activities all together.

Likewise, myocilin homologs can be generated by the present combinatorial approach to selectively inhibit gene expression. For instance, mutagenesis can provide myocilin homologs which are able to bind other signal pathway proteins (or DNA) yet prevent propagation of the signal, e.g. the homologs can be dominant negative mutants.

Moreover, manipulation of certain domains of myocilin by the present method can provide domains more suitable for use in fusion proteins.

In one embodiment, the variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For instance, a mixture of synthetic oligonucleotides can be enzymatically ligated
5 into gene sequences such that the degenerate set of potential GLC1A sequences are expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g. for phage display) containing the set of GLC1A sequences therein.

There are many ways by which such libraries of potential myocilin homologs
10 can be generated from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an appropriate expression vector. The purpose of a degenerate set of genes is to provide, in one mixture, all of the sequences encoding the desired set of potential myocilin sequences. The synthesis of degenerate oligonucleotides
15 is well known in the art (see for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton, Amsterdam: Elsevier ppg. 273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for
20 example, Scott et al. (1990) *Science* 249:386-390; Roberts et al. (1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

Likewise, a library of coding sequence fragments can be provided for a GLC1A clone in order to generate a variegated population of myocilin fragments for
25 screening and subsequent selection of bioactive fragments. A variety of techniques are known in the art for generating such libraries, including chemical synthesis. In one embodiment, a library of coding sequence fragments can be generated by (i) treating a double stranded PCR fragment of a GLC1A coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule; (ii) denaturing the double
30 stranded DNA; (iii) renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products; (iv) removing single stranded portions from reformed duplexes by treatment with S1 nuclease; and (v) ligating the resulting fragment library into an expression vector. By this exemplary method, an expression library

can be derived which codes for N-terminal, C-terminal and internal fragments of various sizes.

A wide range of techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA
5 libraries for gene products having a certain property. Such techniques will be generally adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of GLC1A homologs. The most widely used techniques for screening large gene libraries typically comprises cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing
10 the combinatorial genes under conditions in which detection of a desired activity facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the illustrative assays described below are amenable to high through-put analysis as necessary to screen large numbers of degenerate GLC1A sequences created by combinatorial mutagenesis techniques. Combinatorial mutagenesis has a potential to
15 generate very large libraries of mutant proteins, e.g., in the order of 10^{26} molecules. Combinatorial libraries of this size may be technically challenging to screen even with high throughput screening assays. To overcome this problem, a new technique has been developed recently, recursive ensemble mutagenesis (REM), which allows one to avoid the very high proportion of non-functional proteins in a random library and simply enhances
20 the frequency of functional proteins, thus decreasing the complexity required to achieve a useful sampling of sequence space. REM is an algorithm which enhances the frequency of functional mutants in a library when an appropriate selection or screening method is employed (Arkin and Yourvan, 1992, *PNAS USA* 89:7811-7815; Yourvan et al., 1992, *Parallel Problem Solving from Nature*, 2., In Maenner and Manderick, eds., Elsevir
25 Publishing Co., Amsterdam, pp. 401-410; Delgrave et al., 1993, *Protein Engineering* 6(3):327-331).

The invention also provides for reduction of the myocilin proteins to generate mimetics, e.g. peptide or non-peptide agents, which are able to disrupt binding of a mammalian myocilin polypeptide of the present invention with either upstream or
30 downstream components. Thus, such mutagenic techniques as described above are also useful to map the determinants of the myocilin proteins which participate in protein-protein interactions involved in, for example, binding of the subject myocilin polypeptide to proteins which may function upstream (including both activators and repressors of its activity) or to proteins or nucleic acids which may function downstream of the myocilin

polypeptide, whether they are positively or negatively regulated by it. To illustrate, the critical residues of a subject myocilin polypeptide which are involved in molecular recognition of a component upstream or downstream of myocilin can be determined and used to generate myocilin-derived peptidomimetics which competitively inhibit binding of the authentic myocilin protein with that moiety. By employing, for example, scanning mutagenesis to map the amino acid residues of each of the subject myocilin proteins which are involved in binding other extracellular proteins, peptidomimetic compounds can be generated which mimic those residues of the myocilin protein which facilitate the interaction. Such mimetics may then be used to interfere with the normal function of a myocilin protein. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gamma lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), β -turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans* 1:1231), and b-aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun* 126:419; and Dann et al. (1986) *Biochem Biophys Res Commun* 134:71).

4.4.1. Cells expressing recombinant myocilin polypeptides.

This invention also pertains to a host cell transfected to express a recombinant form of the subject myocilin polypeptides. The host cell may be any prokaryotic or eukaryotic cell. Thus, a nucleotide sequence derived from the cloning of myocilin proteins, encoding all or a selected portion of the full-length protein, can be used to produce a recombinant form of a myocilin polypeptide via microbial or eukaryotic cellular processes. Ligating the polynucleotide sequence into a gene construct, such as an expression vector, and transforming or transfecting into hosts, either eukaryotic (yeast, avian, insect or mammalian) or prokaryotic (bacterial) cells, are standard procedures used in producing other well-known proteins, e.g. MAP kinase, pg. 53, WT1, PTP phosphatases, SRC, and the like. Similar procedures, or modifications thereof, can be employed to

prepare recombinant myocilin polypeptides by microbial means or tissue-culture technology in accord with the subject invention.

The recombinant GLC1A genes can be produced by ligating nucleic acid encoding a myocilin protein, or a portion thereof, into a vector suitable for expression in either prokaryotic cells, eukaryotic cells, or both. Expression vectors for production of recombinant forms of the subject myocilin polypeptides include plasmids and other vectors. For instance, suitable vectors for the expression of a myocilin polypeptide include plasmids of the types: pBR322-derived plasmids, pEMBL-derived plasmids, pEX-derived plasmids, pBTac-derived plasmids and pUC-derived plasmids for expression in prokaryotic cells, such as *E. coli*.

A number of vectors exist for the expression of recombinant proteins in yeast. For instance, YEP24, YIP5, YEP51, YEP52, pYES2, and YRP17 are cloning and expression vehicles useful in the introduction of genetic constructs into *S. cerevisiae* (see, for example, Broach *et al.* (1983) in *Experimental Manipulation of Gene Expression*, ed. M. Inouye Academic Press, p. 83, incorporated by reference herein). These vectors can replicate in *E. coli* due the presence of the pBR322 ori, and in *S. cerevisiae* due to the replication determinant of the yeast 2 micron plasmid. In addition, drug resistance markers such as ampicillin can be used. In an illustrative embodiment, a myocilin polypeptide is produced recombinantly utilizing an expression vector generated by sub-cloning the coding sequence of one of the GLC1A genes represented in SEQ ID Nos: 1-7 or 9.

The preferred mammalian expression vectors contain both prokaryotic sequences, to facilitate the propagation of the vector in bacteria, and one or more eukaryotic transcription units that are expressed in eukaryotic cells. The pcDNAI/amp, pcDNAI/neo, pRc/CMV, pSV2gpt, pSV2neo, pSV2-dhfr, pTk2, pRSVneo, pMSG, pSVT7, pko-neo and pHyg derived vectors are examples of mammalian expression vectors suitable for transfection of eukaryotic cells. Some of these vectors are modified with sequences from bacterial plasmids, such as pBR322, to facilitate replication and drug resistance selection in both prokaryotic and eukaryotic cells. Alternatively, derivatives of viruses such as the bovine papillomavirus (BPV-1), or Epstein-Barr virus (pHEBo, pREP-derived and p205) can be used for transient expression of proteins in eukaryotic cells. The various methods employed in the preparation of the plasmids and transformation of host organisms are well known in the art. For other suitable expression systems for both prokaryotic and eukaryotic cells, as well as general recombinant procedures, see *Molecular Cloning A*

Laboratory Manual, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989) Chapters 16 and 17.

In some instances, it may be desirable to express the recombinant myocilin polypeptide by the use of a baculovirus expression system. Examples of such baculovirus expression systems include pVL-derived vectors (such as pVL1392, pVL1393 and pVL941), pAcUW-derived vectors (such as pAcUW1), and pBlueBac-derived vectors (such as the β -gal containing pBlueBac III).

When it is desirable to express only a portion of a myocilin protein, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from *E. coli* (Ben-Bassat et al. (1987) *J. Bacteriol.* 169:751-757) and *Salmonella typhimurium* and its *in vitro* activity has been demonstrated on recombinant proteins (Miller et al. (1987) *PNAS* 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either *in vivo* by expressing myocilin-derived polypeptides in a host which produces MAP (e.g., *E. coli* or CM89 or *S. cerevisiae*), or *in vitro* by use of purified MAP (e.g., procedure of Miller et al., *supra*).

In other embodiments transgenic animals, described in more detail below could be used to produce recombinant proteins.

4.4.2 Fusion proteins and Immunogens.

In another embodiment, the coding sequences for the polypeptide can be incorporated as a part of a fusion gene including a nucleotide sequence encoding a different polypeptide. This type of expression system can be useful under conditions where it is desirable to produce an immunogenic fragment of a myocilin protein. For example, the VP6 capsid protein of rotavirus can be used as an immunologic carrier protein for portions of the myocilin polypeptide, either in the monomeric form or in the form of a viral particle. The nucleic acid sequences corresponding to the portion of a subject myocilin protein to which antibodies are to be raised can be incorporated into a fusion gene construct which includes coding sequences for a late vaccinia virus structural protein to produce a set of recombinant viruses expressing fusion proteins comprising myocilin epitopes as part of the virion. It has been demonstrated with the use of immunogenic fusion proteins utilizing the

Hepatitis B surface antigen fusion proteins that recombinant Hepatitis B virions can be utilized in this role as well. Similarly, chimeric constructs coding for fusion proteins containing a portion of a myocilin protein and the poliovirus capsid protein can be created to enhance immunogenicity of the set of polypeptide antigens (see, for example, EP
5 Publication No: 0259149; and Evans et al. (1989) *Nature* 339:385; Huang et al. (1988) *J. Virol.* 62:3855; and Schlienger et al. (1992) *J. Virol.* 66:2).

The Multiple Antigen Peptide system for peptide-based immunization can also be utilized to generate an immunogen, wherein a desired portion of a myocilin polypeptide is obtained directly from organo-chemical synthesis of the peptide onto an
10 oligomeric branching lysine core (see, for example, Posnett et al. (1988) *JBC* 263:1719 and Nardelli et al. (1992) *J. Immunol.* 148:914). Antigenic determinants of myocilin proteins can also be expressed and presented by bacterial cells.

In addition to utilizing fusion proteins to enhance immunogenicity, it is widely appreciated that fusion proteins can also facilitate the expression of proteins, and
15 accordingly, can be used in the expression of the myocilin polypeptides of the present invention. For example, myocilin polypeptides can be generated as glutathione-S-transferase (GST-fusion) proteins. Such GST-fusion proteins can enable easy purification of the myocilin polypeptide, as for example by the use of glutathione-derivatized matrices (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel et al. (N.Y.: John
20 Wiley & Sons, 1991)).

In another embodiment, a fusion gene coding for a purification leader sequence, such as a poly-(His)/enterokinase cleavage site sequence at the N-terminus of the desired portion of the recombinant protein, can allow purification of the expressed fusion protein by affinity chromatography using a Ni²⁺ metal resin. The purification leader
25 sequence can then be subsequently removed by treatment with enterokinase to provide the purified protein (e.g., see Hochuli et al. (1987) *J. Chromatography* 411:177; and Janknecht et al. *PNAS* 88:8972). Techniques for making fusion genes are known to those skilled in the art. Essentially, the joining of various DNA fragments coding for different polypeptide sequences is performed in accordance with conventional techniques, employing blunt-ended
30 or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers

which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel et al. John Wiley & Sons: 1992).

5

4.4.3. Antibodies

Another aspect of the invention pertains to an antibody or binding fragment thereof, which is specifically reactive with a myocilin protein. For example, by using immunogens derived from a myocilin protein, e.g. based on the cDNA sequences, anti-protein/anti-peptide antisera or monoclonal antibodies can be made by standard protocols (See, for example, *Antibodies: A Laboratory Manual* ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal, such as a mouse, a hamster or rabbit can be immunized with an immunogenic form of the peptide (e.g., a myocilin polypeptide or an antigenic fragment which is capable of eliciting an antibody response, or a fusion protein as described above). Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of a myocilin protein can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies. In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of a myocilin protein of a mammal, e.g. antigenic determinants of a protein represented by SEQ ID No: 2 or closely related homologs (e.g. at least 92% homologous, and more preferably at least 94% homologous).

Following immunization of an animal with an antigenic preparation of a myocilin polypeptide, anti-myocilin antisera can be obtained and, if desired, polyclonal anti-myocilin antibodies isolated from the serum. To produce monoclonal antibodies, antibody-producing cells (lymphocytes) can be harvested from an immunized animal and fused by standard somatic cell fusion procedures with immortalizing cells such as myeloma cells to yield hybridoma cells. Such techniques are well known in the art, and include, for example, the hybridoma technique (originally developed by Kohler and Milstein, (1975) *Nature*, 256: 495-497), the human B cell hybridoma technique (Kozbar et al., (1983) *Immunology Today*, 4: 72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., (1985) *Monoclonal Antibodies and Cancer*

Therapy, Alan R. Liss, Inc. pp. 77-96). Hybridoma cells can be screened immunochemically for production of antibodies specifically reactive with a myocilin polypeptide of the present invention and monoclonal antibodies isolated from a culture comprising such hybridoma cells.

5 The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with one of the subject mammalian myocilin polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, F(ab)₂ fragments can be generated by treating antibody with
10 pepsin. The resulting F(ab)₂ fragment can be treated to reduce disulfide bridges to produce Fab fragments. The antibody of the present invention is further intended to include bispecific and chimeric molecules having affinity for a myocilin protein conferred by at least one CDR region of the antibody.

 Antibodies which specifically bind myocilin epitopes can also be used in
15 immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of each of the subject myocilin polypeptides. Anti-myocilin antibodies can be used diagnostically in immuno-precipitation and immuno-blotting to detect and evaluate myocilin protein levels in tissue as part of a clinical testing procedure. For instance, such measurements can be useful in predictive valuations of
20 the onset or progression of proliferative disorders. Likewise, the ability to monitor myocilin protein levels in an individual can allow determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of myocilin polypeptides may be measured from cells in bodily fluid, such as in samples of cerebral spinal fluid or amniotic fluid, or can be measured in tissue, such as produced by
25 biopsy. Diagnostic assays using anti-myocilin antibodies can include, for example, immunoassays designed to aid in early diagnosis of a degenerative disorder, particularly ones which are manifest at birth. Diagnostic assays using anti-myocilin polypeptide antibodies can also include immunoassays designed to aid in early diagnosis and phenotyping neoplastic or hyperplastic disorders.

30 Another application of anti-myocilin antibodies of the present invention is in the immunological screening of cDNA libraries constructed in expression vectors such as gt11, gt18-23, ZAP, and ORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, gt11 will produce fusion proteins whose amino termini consist of β-

galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide. Antigenic epitopes of a myocilin protein, e.g. other orthologs of a particular myocilin protein or other paralogs from the same species, can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with
5 anti-myocilin antibodies. Positive phage detected by this assay can then be isolated from the infected plate. Thus, the presence of myocilin homologs can be detected and cloned from other animals, as can alternate isoforms (including splicing variants) from humans.

4.5 Transgenic animals

10 The invention further provides for transgenic animals, which can be used for a variety of purposes, e.g., to identify myocilin therapeutics. Transgenic animals of the invention include non-human animals containing a heterologous GLC1A gene or fragment thereof under the control of a GLC1A promoter or under the control of a heterologous promoter. Accordingly, the transgenic animals of the invention can be animals expressing
15 a transgene encoding a wild-type myocilin protein or fragment thereof or variants thereof, including mutants and polymorphic variants thereof. Such animals can be used, e.g., to determine the effect of a difference in amino acid sequence of a myocilin protein from the sequence set forth in SEQ ID NOS. 8 or 10, such as a polymorphic difference. These animals can also be used to determine the effect of expression of a myocilin protein in a
20 specific site or for identifying myocilin therapeutics or confirming their activity *in vivo*.

The transgenic animals can also be animals containing a transgene, such as reporter gene, under the control of a GLC1A promoter or fragment thereof. These animals are useful, e.g., for identifying drugs that modulate production of myocilin, such as by modulating GLC1A gene expression. A GLC1A gene promoter can be isolated, e.g., by
25 screening of a genomic library with a GLC1A cDNA fragment and characterized according to methods known in the art. In a preferred embodiment of the present invention, the transgenic animal containing said GLC1A reporter gene is used to screen a class of bioactive molecules known as steroid hormones for their ability to modulate GLC1A expression.

30 Yet other non-human animals within the scope of the invention include those in which the expression of the endogenous GLC1A gene has been mutated or "knocked out". A "knock out" animal is one carrying a homozygous or heterozygous deletion of a particular gene or genes. These animals could be used to determine whether the absence of GLC1A will result in a specific phenotype, in particular whether these mice have or are

likely to develop a specific disease, such as high susceptibility to heart disease or cancer. Furthermore these animals are useful in screens for drugs which alleviate or attenuate the disease condition resulting from the mutation of the GLC1A gene as outlined below. These animals are also useful for determining the effect of a specific amino acid difference, or allelic variation, in a GLC1A gene. That is, the GLC1A knock out animals can be crossed with transgenic animals expressing, e.g., a mutated form or allelic variant of GLC1A, thus resulting in an animal which expresses only the mutated protein and not the wild-type myocilin protein.

Methods for obtaining transgenic and knockout non-human animals are well known in the art. Knock out mice are generated by homologous integration of a "knock out" construct into a mouse embryonic stem cell chromosome which encodes the gene to be knocked out. In one embodiment, gene targeting, which is a method of using homologous recombination to modify an animal's genome, can be used to introduce changes into cultured embryonic stem cells. By targeting a GLC1A gene of interest in ES cells, these changes can be introduced into the germlines of animals to generate chimeras. The gene targeting procedure is accomplished by introducing into tissue culture cells a DNA targeting construct that includes a segment homologous to a target GLC1A locus, and which also includes an intended sequence modification to the GLC1A genomic sequence (e.g., insertion, deletion, point mutation). The treated cells are then screened for accurate targeting to identify and isolate those which have been properly targeted.

Gene targeting in embryonic stem cells is in fact a scheme contemplated by the present invention as a means for disrupting a GLC1A gene function through the use of a targeting transgene construct designed to undergo homologous recombination with one or more GLC1A genomic sequences. The targeting construct can be arranged so that, upon recombination with an element of a GLC1A gene, a positive selection marker is inserted into (or replaces) coding sequences of the gene. The inserted sequence functionally disrupts the GLC1A gene, while also providing a positive selection trait. Exemplary GLC1A targeting constructs are described in more detail below.

Generally, the embryonic stem cells (ES cells) used to produce the knockout animals will be of the same species as the knockout animal to be generated. Thus for example, mouse embryonic stem cells will usually be used for generation of knockout mice.

Embryonic stem cells are generated and maintained using methods well known to the skilled artisan such as those described by Doetschman et al. (1985) *J. Embryol. Exp.* 87:27-45). Any line of ES cells can be used, however, the line chosen is

typically selected for the ability of the cells to integrate into and become part of the germ line of a developing embryo so as to create germ line transmission of the knockout construct. Thus, any ES cell line that is believed to have this capability is suitable for use herein. One mouse strain that is typically used for production of ES cells, is the 129J strain.

5 Another ES cell line is murine cell line D3 (American Type Culture Collection, catalog no. CKL 1934) Still another preferred ES cell line is the WW6 cell line (Ioffe et al. (1995) *PNAS* 92:7357-7361). The cells are cultured and prepared for knockout construct insertion using methods well known to the skilled artisan, such as those set forth by Robertson in:

10 *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E.J. Robertson, ed. IRL Press, Washington, D.C. [1987]); by Bradley et al. (1986) *Current Topics in Devel. Biol.* 20:357-371); and by Hogan et al. (*Manipulating the Mouse Embryo: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY [1986]) .

A knock out construct refers to a uniquely configured fragment of nucleic acid which is introduced into a stem cell line and allowed to recombine with the genome

15 at the chromosomal locus of the gene of interest to be mutated. Thus a given knock out construct is specific for a given gene to be targeted for disruption. Nonetheless, many common elements exist among these constructs and these elements are well known in the art. A typical knock out construct contains nucleic acid fragments of not less than about 0.5 kb nor more than about 10.0 kb from both the 5' and the 3' ends of the genomic locus which

20 encodes the gene to be mutated. These two fragments are separated by an intervening fragment of nucleic acid which encodes a positive selectable marker, such as the neomycin resistance gene (neo^R). The resulting nucleic acid fragment, consisting of a nucleic acid from the extreme 5' end of the genomic locus linked to a nucleic acid encoding a positive selectable marker which is in turn linked to a nucleic acid from the extreme 3' end of the

25 genomic locus of interest, omits most of the coding sequence for GLC1A or other gene of interest to be knocked out. When the resulting construct recombines homologously with the chromosome at this locus, it results in the loss of the omitted coding sequence, otherwise known as the structural gene, from the genomic locus. A stem cell in which such a rare homologous recombination event has taken place can be selected for by virtue of the

30 stable integration into the genome of the nucleic acid of the gene encoding the positive selectable marker and subsequent selection for cells expressing this marker gene in the presence of an appropriate drug (neomycin in this example). Variations on this basic technique also exist and are well known in the art. For example, a "knock-in" construct refers to the same basic arrangement of a nucleic acid encoding a 5' genomic locus fragment

linked to nucleic acid encoding a positive selectable marker which in turn is linked to a nucleic acid encoding a 3' genomic locus fragment, but which differs in that none of the coding sequence is omitted and thus the 5' and the 3' genomic fragments used were initially contiguous before being disrupted by the introduction of the nucleic acid encoding the positive selectable marker gene. This "knock-in" type of construct is thus very useful for the construction of mutant transgenic animals when only a limited region of the genomic locus of the gene to be mutated, such as a single exon, is available for cloning and genetic manipulation. Alternatively, the "knock-in" construct can be used to specifically eliminate a single functional domain of the targeted gene, resulting in a transgenic animal which expresses a polypeptide of the targeted gene which is defective in one function, while retaining the function of other domains of the encoded polypeptide. This type of "knock-in" mutant frequently has the characteristic of a so-called "dominant negative" mutant because, especially in the case of proteins which homomultimerize, it can specifically block the action of (or "poison") the polypeptide product of the wild-type gene from which it was derived. In a variation of the knock-in technique, a marker gene is integrated at the genomic locus of interest such that expression of the marker gene comes under the control of the transcriptional regulatory elements of the targeted gene. A marker gene is one that encodes an enzyme whose activity can be detected (e.g., β -galactosidase), the enzyme substrate can be added to the cells under suitable conditions, and the enzymatic activity can be analyzed. One skilled in the art will be familiar with other useful markers and the means for detecting their presence in a given cell. All such markers are contemplated as being included within the scope of the teaching of this invention.

As mentioned above, the homologous recombination of the above described "knock out" and "knock in" constructs is very rare and frequently such a construct inserts nonhomologously into a random region of the genome where it has no effect on the gene which has been targeted for deletion, and where it can potentially recombine so as to disrupt another gene which was otherwise not intended to be altered. Such nonhomologous recombination events can be selected against by modifying the abovementioned knock out and knock in constructs so that they are flanked by negative selectable markers at either end (particularly through the use of two allelic variants of the thymidine kinase gene, the polypeptide product of which can be selected against in expressing cell lines in an appropriate tissue culture medium well known in the art - i.e. one containing a drug such as 5-bromodeoxyuridine). Thus a preferred embodiment of such a knock out or knock in construct of the invention consist of a nucleic acid encoding a negative selectable marker

linked to a nucleic acid encoding a 5' end of a genomic locus linked to a nucleic acid of a positive selectable marker which in turn is linked to a nucleic acid encoding a 3' end of the same genomic locus which in turn is linked to a second nucleic acid encoding a negative selectable marker. Nonhomologous recombination between the resulting knock out construct and the genome will usually result in the stable integration of one or both of these negative selectable marker genes and hence cells which have undergone nonhomologous recombination can be selected against by growth in the appropriate selective media (e.g. media containing a drug such as 5-bromodeoxyuridine for example). Simultaneous selection for the positive selectable marker and against the negative selectable marker will result in a vast enrichment for clones in which the knock out construct has recombined homologously at the locus of the gene intended to be mutated. The presence of the predicted chromosomal alteration at the targeted gene locus in the resulting knock out stem cell line can be confirmed by means of Southern blot analytical techniques which are well known to those familiar in the art. Alternatively, PCR can be used.

Each knockout construct to be inserted into the cell must first be in the linear form. Therefore, if the knockout construct has been inserted into a vector (described *infra*), linearization is accomplished by digesting the DNA with a suitable restriction endonuclease selected to cut only within the vector sequence and not within the knockout construct sequence.

For insertion, the knockout construct is added to the ES cells under appropriate conditions for the insertion method chosen, as is known to the skilled artisan. For example, if the ES cells are to be electroporated, the ES cells and knockout construct DNA are exposed to an electric pulse using an electroporation machine and following the manufacturer's guidelines for use. After electroporation, the ES cells are typically allowed to recover under suitable incubation conditions. The cells are then screened for the presence of the knock out construct as explained above. Where more than one construct is to be introduced into the ES cell, each knockout construct can be introduced simultaneously or one at a time.

After suitable ES cells containing the knockout construct in the proper location have been identified by the selection techniques outlined above, the cells can be inserted into an embryo. Insertion may be accomplished in a variety of ways known to the skilled artisan, however a preferred method is by microinjection. For microinjection, about 10-30 cells are collected into a micropipet and injected into embryos that are at the proper stage of development to permit integration of the foreign ES cell containing the knockout

construct into the developing embryo. For instance, the transformed ES cells can be microinjected into blastocytes. The suitable stage of development for the embryo used for insertion of ES cells is very species dependent, however for mice it is about 3.5 days. The embryos are obtained by perfusing the uterus of pregnant females. Suitable methods for accomplishing this are known to the skilled artisan, and are set forth by, e.g., Bradley et al. (supra).

While any embryo of the right stage of development is suitable for use, preferred embryos are male. In mice, the preferred embryos also have genes coding for a coat color that is different from the coat color encoded by the ES cell genes. In this way, the offspring can be screened easily for the presence of the knockout construct by looking for mosaic coat color (indicating that the ES cell was incorporated into the developing embryo). Thus, for example, if the ES cell line carries the genes for white fur, the embryo selected will carry genes for black or brown fur.

After the ES cell has been introduced into the embryo, the embryo may be implanted into the uterus of a pseudopregnant foster mother for gestation. While any foster mother may be used, the foster mother is typically selected for her ability to breed and reproduce well, and for her ability to care for the young. Such foster mothers are typically prepared by mating with vasectomized males of the same species. The stage of the pseudopregnant foster mother is important for successful implantation, and it is species dependent. For mice, this stage is about 2-3 days pseudopregnant.

Offspring that are born to the foster mother may be screened initially for mosaic coat color where the coat color selection strategy (as described above, and in the appended examples) has been employed. In addition, or as an alternative, DNA from tail tissue of the offspring may be screened for the presence of the knockout construct using Southern blots and/or PCR as described above. Offspring that appear to be mosaics may then be crossed to each other, if they are believed to carry the knockout construct in their germ line, in order to generate homozygous knockout animals. Homozygotes may be identified by Southern blotting of equivalent amounts of genomic DNA from mice that are the product of this cross, as well as mice that are known heterozygotes and wild type mice.

Other means of identifying and characterizing the knockout offspring are available. For example, Northern blots can be used to probe the mRNA for the presence or absence of transcripts encoding either the gene knocked out, the marker gene, or both. In addition, Western blots can be used to assess the level of expression of the GLC1A gene knocked out in various tissues of the offspring by probing the Western blot with an antibody

against the particular myocilin protein, or an antibody against the marker gene product, where this gene is expressed. Finally, *in situ* analysis (such as fixing the cells and labeling with antibody) and/or FACS (fluorescence activated cell sorting) analysis of various cells from the offspring can be conducted using suitable antibodies to look for the presence or
5 absence of the knockout construct gene product.

Yet other methods of making knock-out or disruption transgenic animals are also generally known. See, for example, *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Recombinase dependent knockouts can also be generated, e.g. by homologous recombination to insert target
10 sequences, such that tissue specific and/or temporal control of inactivation of a GLC1A-gene can be controlled by recombinase sequences (described *infra*).

Animals containing more than one knockout construct and/or more than one transgene expression construct are prepared in any of several ways. The preferred manner of preparation is to generate a series of mammals, each containing one of the desired
15 transgenic phenotypes. Such animals are bred together through a series of crosses, backcrosses and selections, to ultimately generate a single animal containing all desired knockout constructs and/or expression constructs, where the animal is otherwise congenic (genetically identical) to the wild type except for the presence of the knockout construct(s) and/or transgene(s).

20 A GLC1A transgene can encode the wild-type form of the protein, or can encode homologs thereof, including both agonists and antagonists, as well as antisense constructs. In preferred embodiments, the expression of the transgene is restricted to specific subsets of cells, tissues or developmental stages utilizing, for example, cis-acting sequences that control expression in the desired pattern. In the present invention, such
25 mosaic expression of a myocilin protein can be essential for many forms of lineage analysis and can additionally provide a means to assess the effects of, for example, lack of GLC1A expression which might grossly alter development in small patches of tissue within an otherwise normal embryo. Toward this end, tissue-specific regulatory sequences and conditional regulatory sequences can be used to control expression of the transgene in
30 certain spatial patterns. Moreover, temporal patterns of expression can be provided by, for example, conditional recombination systems or prokaryotic transcriptional regulatory sequences.

Genetic techniques, which allow for the expression of transgenes can be regulated via site-specific genetic manipulation *in vivo*, are known to those skilled in the art.

For instance, genetic systems are available which allow for the regulated expression of a recombinase that catalyzes the genetic recombination of a target sequence. As used herein, the phrase "target sequence" refers to a nucleotide sequence that is genetically recombined by a recombinase. The target sequence is flanked by recombinase recognition sequences and is generally either excised or inverted in cells expressing recombinase activity. Recombinase catalyzed recombination events can be designed such that recombination of the target sequence results in either the activation or repression of expression of one of the subject myocilin proteins. For example, excision of a target sequence which interferes with the expression of a recombinant GLC1A gene, such as one which encodes an antagonistic homolog or an antisense transcript, can be designed to activate expression of that gene. This interference with expression of the protein can result from a variety of mechanisms, such as spatial separation of the GLC1A gene from the promoter element or an internal stop codon. Moreover, the transgene can be made wherein the coding sequence of the gene is flanked by recombinase recognition sequences and is initially transfected into cells in a 3' to 5' orientation with respect to the promoter element. In such an instance, inversion of the target sequence will reorient the subject gene by placing the 5' end of the coding sequence in an orientation with respect to the promoter element which allow for promoter driven transcriptional activation.

The transgenic animals of the present invention all include within a plurality of their cells a transgene of the present invention, which transgene alters the phenotype of the "host cell" with respect to regulation of cell growth, death and/or differentiation. Since it is possible to produce transgenic organisms of the invention utilizing one or more of the transgene constructs described herein, a general description will be given of the production of transgenic organisms by referring generally to exogenous genetic material. This general description can be adapted by those skilled in the art in order to incorporate specific transgene sequences into organisms utilizing the methods and materials described below.

In an illustrative embodiment, either the *cre/loxP* recombinase system of bacteriophage P1 (Lakso et al. (1992) *PNAS* 89:6232-6236; Orban et al. (1992) *PNAS* 89:6861-6865) or the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman et al. (1991) *Science* 251:1351-1355; PCT publication WO 92/15694) can be used to generate *in vivo* site-specific genetic recombination systems. Cre recombinase catalyzes the site-specific recombination of an intervening target sequence located between *loxP* sequences. *loxP* sequences are 34 base pair nucleotide repeat sequences to which the Cre recombinase binds and are required for Cre recombinase mediated genetic recombination.

The orientation of *loxP* sequences determines whether the intervening target sequence is excised or inverted when Cre recombinase is present (Abremski et al. (1984) *J. Biol. Chem.* 259:1509-1514); catalyzing the excision of the target sequence when the *loxP* sequences are oriented as direct repeats and catalyzes inversion of the target sequence when *loxP* sequences are oriented as inverted repeats.

Accordingly, genetic recombination of the target sequence is dependent on expression of the Cre recombinase. Expression of the recombinase can be regulated by promoter elements which are subject to regulatory control, e.g., tissue-specific, developmental stage-specific, inducible or repressible by externally added agents. This regulated control will result in genetic recombination of the target sequence only in cells where recombinase expression is mediated by the promoter element. Thus, the activation expression of a recombinant myocilin protein can be regulated via control of recombinase expression.

Use of the *cre/loxP* recombinase system to regulate expression of a recombinant myocilin protein requires the construction of a transgenic animal containing transgenes encoding both the Cre recombinase and the subject protein. Animals containing both the Cre recombinase and a recombinant GLC1A gene can be provided through the construction of "double" transgenic animals. A convenient method for providing such animals is to mate two transgenic animals each containing a transgene, e.g., a GLC1A gene and recombinase gene.

Similar conditional transgenes can be provided using prokaryotic promoter sequences which require prokaryotic proteins to be simultaneously expressed in order to facilitate expression of the GLC1A transgene. Exemplary promoters and the corresponding trans-activating prokaryotic proteins are given in U.S. Patent No. 4,833,080.

Moreover, expression of the conditional transgenes can be induced by gene therapy-like methods wherein a gene encoding the trans-activating protein, e.g. a recombinase or a prokaryotic protein, is delivered to the tissue and caused to be expressed, such as in a cell-type specific manner. By this method, a GLC1A transgene could remain silent into adulthood until "turned on" by the introduction of the trans-activator.

In an exemplary embodiment, the "transgenic non-human animals" of the invention are produced by introducing transgenes into the germline of the non-human animal. Embryonal target cells at various developmental stages can be used to introduce transgenes. Different methods are used depending on the stage of development of the embryonal target cell. The specific line(s) of any animal used to practice this invention are

selected for general good health, good embryo yields, good pronuclear visibility in the embryo, and good reproductive fitness. In addition, the haplotype is a significant factor. For example, when transgenic mice are to be produced, strains such as C57BL/6 or FVB lines are often used (Jackson Laboratory, Bar Harbor, ME). Preferred strains are those with H-2^b,
5 H-2^d or H-2^q haplotypes such as C57BL/6 or DBA/1. The line(s) used to practice this invention may themselves be transgenics, and/or may be knockouts (i.e., obtained from animals which have one or more genes partially or completely suppressed) .

In one embodiment, the transgene construct is introduced into a single stage embryo. The zygote is the best target for micro-injection. In the mouse, the male
10 pronucleus reaches the size of approximately 20 micrometers in diameter which allows reproducible injection of 1-2pl of DNA solution. The use of zygotes as a target for gene transfer has a major advantage in that in most cases the injected DNA will be incorporated into the host gene before the first cleavage (Brinster et al. (1985) *PNAS* 82:4438-4442). As a consequence, all cells of the transgenic animal will carry the incorporated transgene. This
15 will in general also be reflected in the efficient transmission of the transgene to offspring of the founder since 50% of the germ cells will harbor the transgene.

Normally, fertilized embryos are incubated in suitable media until the pronuclei appear. At about this time, the nucleotide sequence comprising the transgene is introduced into the female or male pronucleus as described below. In some species such
20 as mice, the male pronucleus is preferred. It is most preferred that the exogenous genetic material be added to the male DNA complement of the zygote prior to its being processed by the ovum nucleus or the zygote female pronucleus. It is thought that the ovum nucleus or female pronucleus release molecules which affect the male DNA complement, perhaps by replacing the protamines of the male DNA with histones, thereby facilitating the
25 combination of the female and male DNA complements to form the diploid zygote.

Thus, it is preferred that the exogenous genetic material be added to the male complement of DNA or any other complement of DNA prior to its being affected by the female pronucleus. For example, the exogenous genetic material is added to the early male pronucleus, as soon as possible after the formation of the male pronucleus, which is when
30 the male and female pronuclei are well separated and both are located close to the cell membrane. Alternatively, the exogenous genetic material could be added to the nucleus of the sperm after it has been induced to undergo decondensation. Sperm containing the exogenous genetic material can then be added to the ovum or the decondensed sperm could

be added to the ovum with the transgene constructs being added as soon as possible thereafter.

Introduction of the transgene nucleotide sequence into the embryo may be accomplished by any means known in the art such as, for example, microinjection, electroporation, or lipofection. Following introduction of the transgene nucleotide sequence into the embryo, the embryo may be incubated *in vitro* for varying amounts of time, or reimplanted into the surrogate host, or both. In vitro incubation to maturity is within the scope of this invention. One common method is to incubate the embryos in vitro for about 1-7 days, depending on the species, and then reimplant them into the surrogate host.

For the purposes of this invention a zygote is essentially the formation of a diploid cell which is capable of developing into a complete organism. Generally, the zygote will be comprised of an egg containing a nucleus formed, either naturally or artificially, by the fusion of two haploid nuclei from a gamete or gametes. Thus, the gamete nuclei must be ones which are naturally compatible, i.e., ones which result in a viable zygote capable of undergoing differentiation and developing into a functioning organism. Generally, a euploid zygote is preferred. If an aneuploid zygote is obtained, then the number of chromosomes should not vary by more than one with respect to the euploid number of the organism from which either gamete originated.

In addition to similar biological considerations, physical ones also govern the amount (e.g., volume) of exogenous genetic material which can be added to the nucleus of the zygote or to the genetic material which forms a part of the zygote nucleus. If no genetic material is removed, then the amount of exogenous genetic material which can be added is limited by the amount which will be absorbed without being physically disruptive. Generally, the volume of exogenous genetic material inserted will not exceed about 10 picoliters. The physical effects of addition must not be so great as to physically destroy the viability of the zygote. The biological limit of the number and variety of DNA sequences will vary depending upon the particular zygote and functions of the exogenous genetic material and will be readily apparent to one skilled in the art, because the genetic material, including the exogenous genetic material, of the resulting zygote must be biologically capable of initiating and maintaining the differentiation and development of the zygote into a functional organism.

The number of copies of the transgene constructs which are added to the zygote is dependent upon the total amount of exogenous genetic material added and will be the amount which enables the genetic transformation to occur. Theoretically only one copy

is required; however, generally, numerous copies are utilized, for example, 1,000-20,000 copies of the transgene construct, in order to insure that one copy is functional. As regards the present invention, there will often be an advantage to having more than one functioning copy of each of the inserted exogenous DNA sequences to enhance the phenotypic expression of the exogenous DNA sequences.

Any technique which allows for the addition of the exogenous genetic material into nucleic genetic material can be utilized so long as it is not destructive to the cell, nuclear membrane or other existing cellular or genetic structures. The exogenous genetic material is preferentially inserted into the nucleic genetic material by microinjection. Microinjection of cells and cellular structures is known and is used in the art.

Reimplantation is accomplished using standard methods. Usually, the surrogate host is anesthetized, and the embryos are inserted into the oviduct. The number of embryos implanted into a particular host will vary by species, but will usually be comparable to the number of off spring the species naturally produces.

Transgenic offspring of the surrogate host may be screened for the presence and/or expression of the transgene by any suitable method. Screening is often accomplished by Southern blot or Northern blot analysis, using a probe that is complementary to at least a portion of the transgene. Western blot analysis using an antibody against the protein encoded by the transgene may be employed as an alternative or additional method for screening for the presence of the transgene product. Typically, DNA is prepared from tail tissue and analyzed by Southern analysis or PCR for the transgene. Alternatively, the tissues or cells believed to express the transgene at the highest levels are tested for the presence and expression of the transgene using Southern analysis or PCR, although any tissues or cell types may be used for this analysis.

Alternative or additional methods for evaluating the presence of the transgene include, without limitation, suitable biochemical assays such as enzyme and/or immunological assays, histological stains for particular marker or enzyme activities, flow cytometric analysis, and the like. Analysis of the blood may also be useful to detect the presence of the transgene product in the blood, as well as to evaluate the effect of the transgene on the levels of various types of blood cells and other blood constituents.

Progeny of the transgenic animals may be obtained by mating the transgenic animal with a suitable partner, or by *in vitro* fertilization of eggs and/or sperm obtained from the transgenic animal. Where mating with a partner is to be performed, the partner may or may not be transgenic and/or a knockout; where it is transgenic, it may contain the

same or a different transgene, or both. Alternatively, the partner may be a parental line. Where *in vitro* fertilization is used, the fertilized embryo may be implanted into a surrogate host or incubated *in vitro*, or both. Using either method, the progeny may be evaluated for the presence of the transgene using methods described above, or other appropriate methods.

5 The transgenic animals produced in accordance with the present invention will include exogenous genetic material. As set out above, the exogenous genetic material will, in certain embodiments, be a DNA sequence which results in the production of a myocilin protein (either agonistic or antagonistic), and antisense transcript, or a myocilin mutant. Further, in such embodiments the sequence will be attached to a transcriptional
10 control element, e.g., a promoter, which preferably allows the expression of the transgene product in a specific type of cell.

Retroviral infection can also be used to introduce transgene into a non-human animal. The developing non-human embryo can be cultured *in vitro* to the blastocyst stage. During this time, the blastomeres can be targets for retroviral infection (Jaenich, R.
15 (1976) *PNAS* 73:1260-1264). Efficient infection of the blastomeres is obtained by enzymatic treatment to remove the zona pellucida (*Manipulating the Mouse Embryo*, Hogan eds. (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 1986). The viral vector system used to introduce the transgene is typically a replication-defective retrovirus carrying the transgene (Jahner et al. (1985) *PNAS* 82:6927-6931; Van der Putten et al.
20 (1985) *PNAS* 82:6148-6152). Transfection is easily and efficiently obtained by culturing the blastomeres on a monolayer of virus-producing cells (Van der Putten, *supra*; Stewart et al. (1987) *EMBO J.* 6:383-388). Alternatively, infection can be performed at a later stage. Virus or virus-producing cells can be injected into the blastocoele (Jahner et al. (1982) *Nature* 298:623-628). Most of the founders will be mosaic for the transgene since
25 incorporation occurs only in a subset of the cells which formed the transgenic non-human animal. Further, the founder may contain various retroviral insertions of the transgene at different positions in the genome which generally will segregate in the offspring. In addition, it is also possible to introduce transgenes into the germ line by intrauterine retroviral infection of the midgestation embryo (Jahner et al. (1982) *supra*).

30 A third type of target cell for transgene introduction is the embryonal stem cell (ES). ES cells are obtained from pre-implantation embryos cultured *in vitro* and fused with embryos (Evans et al. (1981) *Nature* 292:154-156; Bradley et al. (1984) *Nature* 309:255-258; Gossler et al. (1986) *PNAS* 83: 9065-9069; and Robertson et al. (1986) *Nature* 322:445-448). Transgenes can be efficiently introduced into the ES cells by DNA

transfection or by retrovirus-mediated transduction. Such transformed ES cells can thereafter be combined with blastocysts from a non-human animal. The ES cells thereafter colonize the embryo and contribute to the germ line of the resulting chimeric animal. For review see Jaenisch, R. (1988) *Science* 240:1468-1474.

5

4.6. Drug Screening Assays for GLC1A Therapeutics

Based on the discovery of the GLC1A gene and specific mutations in the gene that correlate with the existence of glaucoma, one of skill in the art is able to use any of a variety of standard assays to screen for drugs, which will interfere with or otherwise prevent the development of glaucoma. By addressing the molecular basis of glaucoma, these agents are expected to be superior to existing therapies.

For example, identification of the precise phenotype associated with these mutations can be used to identify functionally important regions of the protein. These specific mutations can then be used in other experiments which will include overexpression in cell lines and the creation of transgenic animals. Ideally, one could identify mutations which reproducibly cause glaucoma at very different times in the person's life and then be able to show that these mutations had similar differences of effect in a cellular expression system or a transgenic animal.

In addition, proteins that interact with the GLC1A gene product and genes encoding the proteins can now be identified, since proteins that interact with GLC1A gene product will be important targets for involvement in the pathogenesis of various types of glaucoma.

Further, studies will be undertaken to discover whether mutations known to cause glaucoma in human beings alter protein trafficking in tissue culture as well as animal models, since one mechanism through which mutations in the GLC1A gene could cause disease would be to alter the expression of other important gene products. This can occur by affecting overall protein trafficking within the cell caused for example by increased removal of mutant proteins at the level of the endoplasmic reticulum.

Further understanding of the pathogenesis of glaucoma is useful for identifying new classes of drugs which can be useful in the treatment of glaucoma. For example, the GLC1A gene has been found to be induced by exposure of cells to steroids. Therefore, drugs which are capable of blocking this steroid effect should prove useful for preventing or delaying the development of glaucoma.

As further described below, *in vitro* assays which are suitable for very high throughput screening of compounds can be performed. As the simplest example of this approach, one could use antibodies to the GLC1A gene product to develop a simple ELISA assay for the induction of the GLC1A gene product and then perform this assay
5 in a 96 well microtiter plate format to screen a large number of drugs for the efficacy in blocking the steroid induction of the gene product. In this way, automated methods could be used to screen several thousand potentially therapeutic compounds for efficacy.

Also, knowledge of the structure/function of the GLC1A gene immediately suggests other genes which might be involved in glaucoma. Such clues
10 will come from studies of homology, evolution, evaluation of structural motifs within the gene, and genetic studies using analyses designed to identify genes causing polygenic disease.

In the original linkage study described herein, it was recognized that 3 of 22 obligate carriers of the glaucoma gene failed to manifest a severe glaucoma
15 phenotype. This information suggests that other genes are capable of mitigating the effect of the GLC1A mutation. One powerful way to search for such mitigator genes is to express a glaucoma-causing gene in different backgrounds. This can be done by creating transgenic animals and then breeding the glaucoma-causing gene on different genetic mouse strains. If the phenotype is altered in different strains these animals can
20 be back crossed in such a way that the mitigating gene can be identified.

Some of the assays mentioned above, will now be described in further detail below.

25 4.6.1 Cell-free assays

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins, are often preferred
30 as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an

alteration of binding affinity with upstream or downstream elements. Accordingly, in an exemplary screening assay of the present invention, the compound of interest is contacted with proteins which may function upstream (including both activators and repressors of its activity) or to proteins or nucleic acids which may function downstream of the myocilin polypeptide, whether they are positively or negatively regulated by it. To the mixture of the compound and the upstream or downstream element is then added a composition containing a myocilin polypeptide. Detection and quantification of complexes of myocilin with its upstream or downstream elements provide a means for determining a compound's efficacy at inhibiting (or potentiating) complex formation between myocilin and a myocilin-binding element. The efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. In the control assay, isolated and purified myocilin polypeptide is added to a composition containing the myocilin-binding element, and the formation of a complex is quantitated in the absence of the test compound.

Complex formation between the myocilin polypeptide and a myocilin binding element may be detected by a variety of techniques. Modulation of the formation of complexes can be quantitated using, for example, detectably labeled proteins such as radiolabeled, fluorescently labeled, or enzymatically labeled myocilin polypeptides, by immunoassay, or by chromatographic detection.

Typically, it will be desirable to immobilize either myocilin or its binding protein to facilitate separation of complexes from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of myocilin to an upstream or downstream element, in the presence and absence of a candidate agent, can be accomplished in any vessel suitable for containing the reactants. Examples include microtitre plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided which adds a domain that allows the protein to be bound to a matrix. For example, glutathione-S-transferase/myocilin (GST/myocilin) fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtitre plates, which are then combined with the cell lysates, e.g. an ^{35}S -labeled, and the test compound, and the mixture incubated under conditions conducive to complex formation, e.g. at physiological conditions for salt and pH, though slightly more stringent conditions may be desired. Following incubation, the beads are washed to remove any unbound label, and the matrix immobilized and radiolabel

determined directly (e.g. beads placed in scintillant), or in the supernatant after the complexes are subsequently dissociated. Alternatively, the complexes can be dissociated from the matrix, separated by SDS-PAGE, and the level of myocilin-binding protein found in the bead fraction quantitated from the gel using standard electrophoretic techniques such as described in the appended examples.

Other techniques for immobilizing proteins on matrices are also available for use in the subject assay. For instance, either myocilin or its cognate binding protein can be immobilized utilizing conjugation of biotin and streptavidin. For instance, biotinylated myocilin molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with myocilin but which do not interfere with binding of upstream or downstream elements can be derivatized to the wells of the plate, and myocilin trapped in the wells by antibody conjugation. As above, preparations of a myocilin-binding protein and a test compound are incubated in the myocilin-presenting wells of the plate, and the amount of complex trapped in the well can be quantitated. Exemplary methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the myocilin binding element, or which are reactive with myocilin protein and compete with the binding element; as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the binding element, either intrinsic or extrinsic activity. In the instance of the latter, the enzyme can be chemically conjugated or provided as a fusion protein with the myocilin-BP. To illustrate, the myocilin-BP can be chemically cross-linked or genetically fused with horseradish peroxidase, and the amount of polypeptide trapped in the complex can be assessed with a chromogenic substrate of the enzyme, e.g. 3,3'-diamino-benzadine tetrahydrochloride or 4-chloro-1-naphthol. Likewise, a fusion protein comprising the polypeptide and glutathione-S-transferase can be provided, and complex formation quantitated by detecting the GST activity using 1-chloro-2,4-dinitrobenzene (Habig et al (1974) J Biol Chem 249:7130).

For processes which rely on immunodetection for quantitating one of the proteins trapped in the complex, antibodies against the protein, such as anti-myocilin antibodies, can be used. Alternatively, the protein to be detected in the complex can be "epitope tagged" in the form of a fusion protein which includes, in addition to the myocilin sequence, a second polypeptide for which antibodies are readily available (e.g. from

commercial sources). For instance, the GST fusion proteins described above can also be used for quantification of binding using antibodies against the GST moiety. Other useful epitope tags include myc-epitopes (e.g., see Ellison et al. (1991) J Biol Chem 266:21150-21157) which includes a 10-residue sequence from c-myc, as well as the pFLAG system (International Biotechnologies, Inc.) or the pEZZ-protein A system (Pharmacia, NJ).

4.6.2. Cell based assays

In addition to cell-free assays, such as described above, the readily available source of mutant and functional GLC1A nucleic acids and proteins provided by the present invention also facilitates the generation of cell-based assays for identifying small molecule agonists/antagonists and the like. For example, cells can be caused to overexpress a recombinant myocilin protein in the presence and absence of a test agent of interest, with the assay scoring for modulation in myocilin responses by the target cell mediated by the test agent. As with the cell-free assays, agents which produce a statistically significant change in myocilin-dependent responses (either inhibition or potentiation) can be identified. In an illustrative embodiment, the expression or activity of a myocilin is modulated in cells and the effects of compounds of interest on the readout of interest (such as tissue differentiation, proliferation, tumorigenesis) are measured. For example, the expression of genes which are up- or down-regulated in response to a myocilin-dependent signal cascade can be assayed. In preferred embodiments, the regulatory regions of such genes, e.g., the 5' flanking promoter and enhancer regions, are operably linked to a detectable marker (such as luciferase) which encodes a gene product that can be readily detected.

Exemplary cells or cell lines may be derived from ocular tissue (e.g. trabecular meshwork or ciliary body epithelia); as well as generic mammalian cell lines such as HeLa cells and COS cells, e.g., COS-7 (ATCC# CRL-1651). Further, the transgenic animals discussed herein may be used to generate cell lines containing one or more cell types involved in glaucoma, that can be used as cell culture models for this disorder. While primary cultures derived from the glaucomatous transgenic animals of the invention may be utilized, the generation of continuous cell lines is preferred. For examples of techniques which may be used to derive a continuous cell line from the transgenic animals, see Small et al., 1985, Mol. Cell Biol. 5:642-648.

Using these cells, the effect of a test compound on a variety of end points can be tested including cell proliferation, migration, phagocytosis, adherence and/or biosynthesis (e.g. of extracellular matrix components). The cells can then be examined for

phenotypes associated with glaucoma, including, but not limited to changes in cellular morphology, cell proliferation, cell migration, and cell adhesion.

In the event that the myocilin proteins themselves, or in complexes with other proteins, are capable of binding DNA and modifying transcription of a gene, a transcriptional based assay could be used, for example, in which a myocilin responsive regulatory sequence is operably linked to a detectable marker gene.

Monitoring the influence of compounds on cells may be applied not only in basic drug screening, but also in clinical trials. In such clinical trials, the expression of a panel of genes may be used as a "read out" of a particular drug's therapeutic effect.

In yet another aspect of the invention, the subject myocilin polypeptides can be used to generate a "two hybrid" assay (see, for example, U.S. Patent No. 5,283,317; Zervos et al. (1993) Cell 72:223-232; Madura et al. (1993) J Biol Chem 268:12046-12054; Bartel et al. (1993) Biotechniques 14:920-924; Iwabuchi et al. (1993) Oncogene 8:1693-1696; and Brent WO94/10300), for isolating coding sequences for other cellular proteins which bind to or interact with myocilin ("myocilin-binding proteins" or "myocilin-bp").

Briefly, the two hybrid assay relies on reconstituting *in vivo* a functional transcriptional activator protein from two separate fusion proteins. In particular, the method makes use of chimeric genes which express hybrid proteins. To illustrate, a first hybrid gene comprises the coding sequence for a DNA-binding domain of a transcriptional activator fused in frame to the coding sequence for a myocilin polypeptide. The second hybrid protein encodes a transcriptional activation domain fused in frame to a sample gene from a cDNA library. If the bait and sample hybrid proteins are able to interact, e.g., form a myocilin-dependent complex, they bring into close proximity the two domains of the transcriptional activator. This proximity is sufficient to cause transcription of a reporter gene which is operably linked to a transcriptional regulatory site responsive to the transcriptional activator, and expression of the reporter gene can be detected and used to score for the interaction of the myocilin and sample proteins.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

4.7 Methods of Treating Disease

In addition to glaucoma, there may be a variety of pathological conditions for which myocilin therapeutics of the present invention can be used in treatment.

A "myocilin therapeutic," whether an antagonist or agonist of wild type myocilin, can be, as appropriate, any of the preparations described above, including isolated polypeptides, gene therapy constructs, antisense molecules, peptidomimetics, non-nucleic acid, non-peptidic small molecules, or agents identified in the drug assays provided herein.

5 As described herein, subjects having certain mutant GLC1A genes tend to develop glaucoma. Down-regulation of mutant GLC1A gene expression and/or a resultant decrease in the activity of a mutant myocilin protein (e.g. using antisense, ribozyme, triple helix or antibody molecules) and/or up-regulation of a wildtype GLC1A gene expression and/or a resultant increase in the activity of a wildtype myocilin protein (e.g. using gene
10 therapy or protein replacement therapies) should therefore prove useful in ameliorating disease symptoms. Compounds identified as increasing or decreasing GLC1A gene expression or myocilin protein activity can be administered to a subject at therapeutically effective dose to treat or ameliorate symptoms associated with glaucoma.

15 4.7.1. Effective Dose

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and
20 therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Compounds which exhibit large therapeutic indices are preferred. While compounds that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

25 The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method
30 of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC₅₀ (i.e., the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such

information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

4.7.2. Formulation and Use

5 Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients. Thus, the compounds and their physiologically acceptable salts and solvates may be formulated for administration by, for example, injection, inhalation or insufflation (either through the mouth or the nose) or oral, buccal, parenteral
10 or rectal administration.

 For such therapy, the oligomers of the invention can be formulated for a variety of loads of administration, including systemic and topical or localized administration. Techniques and formulations generally may be found in *Remington's Pharmaceutical Sciences*, Meade Publishing Co., Easton, PA. For systemic administration,
15 injection is preferred, including intramuscular, intravenous, intraperitoneal, and subcutaneous. For injection, the oligomers of the invention can be formulated in liquid solutions, preferably in physiologically compatible buffers such as Hank's solution or Ringer's solution. In addition, the oligomers may be formulated in solid form and redissolved or suspended immediately prior to use. Lyophilized forms are also included.

20 For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (*e.g.*, pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (*e.g.*, lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (*e.g.*, magnesium
25 stearate, talc or silica); disintegrants (*e.g.*, potato starch or sodium starch glycolate); or wetting agents (*e.g.*, sodium lauryl sulphate). The tablets may be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may
30 be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (*e.g.*, sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (*e.g.*, lecithin or acacia); non-aqueous vehicles (*e.g.*, almond oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (*e.g.*, methyl or

propyl-p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate.

Preparations for oral administration may be suitably formulated to give controlled release of the active compound.

5 For buccal administration the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*,
10 dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of *e.g.* gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

15 The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampoules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as
20 suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as
25 cocoa butter or other glycerides.

In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with
30 suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be

permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration bile salts and fusidic acid derivatives. In addition, detergents may be used to facilitate permeation. Transmucosal administration may be through nasal sprays or using suppositories. For topical administration, the oligomers of the invention are formulated into ointments, salves, gels, or creams as generally known in the art.

In clinical settings, the gene delivery systems for the therapeutic GLC1A gene can be introduced into a patient by any of a number of methods, each of which is familiar in the art. For instance, a pharmaceutical preparation of the gene delivery system can be introduced systemically, e.g. by intravenous injection, and specific transduction of the protein in the target cells occurs predominantly from specificity of transfection provided by the gene delivery vehicle, cell-type or tissue-type expression due to the transcriptional regulatory sequences controlling expression of the receptor gene, or a combination thereof. In other embodiments, initial delivery of the recombinant gene is more limited with introduction into the animal being quite localized. For example, the gene delivery vehicle can be introduced by catheter (see U.S. Patent 5,328,470) or by stereotactic injection (e.g. Chen et al. (1994) *PNAS* 91: 3054-3057). A GLC1A gene, such as any one of the sequences represented in the group consisting of SEQ ID NO: 1 or 2, or a sequence homologous thereto can be delivered in a gene therapy construct by electroporation using techniques described, for example, by Dev et al. ((1994) *Cancer Treat Rev* 20:105-115). Gene therapy vectors comprised of viruses that provide specific effective and highly localized treatment of eye diseases are described in Published International Patent Application No. WO 95/34580 to U. Eriksson et al..

The pharmaceutical preparation of the gene therapy construct can consist essentially of the gene delivery system in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery system can be produced intact from recombinant cells, e.g. retroviral vectors, the pharmaceutical preparation can comprise one or more cells which produce the gene delivery system.

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

4.8 Predictive Medicine

The invention further features predictive medicines, which are based, at least in part, on the identity of the novel GLC1A genes and alterations in the genes and related pathway genes, which affect the expression level and/or function of the encoded myocilin protein in a subject.

For example, information obtained using the diagnostic assays described herein (alone or in conjunction with information on another genetic defect, which contributes to the same disease) is useful for diagnosing or confirming that a symptomatic subject (e.g. a subject symptomatic for glaucoma), has a genetic defect (e.g. in a GLC1A gene or in a gene that regulates the expression of an GLC1A gene), which causes or contributes to glaucoma. Alternatively, the information (alone or in conjunction with information on another genetic defect, which contributes to the same disease) can be used prognostically for predicting whether a non-symptomatic subject is likely to develop glaucoma. Based on the prognostic information, a doctor can recommend a regimen or therapeutic protocol, useful for preventing or prolonging onset of glaucoma in the individual.

In addition, knowledge of the particular alteration or alterations resulting in defective or deficient GLC1A genes or proteins in an individual (the GLC1A genetic profile), alone or in conjunction with information on other genetic defects contributing to glaucoma (the genetic profile of glaucoma) allows customization of therapy to the individual's genetic profile, the goal of "pharmacogenomics". For example, an individual's GLC1A genetic profile or the genetic profile of glaucoma, can enable a doctor to: 1) more effectively prescribe a drug that will address the molecular basis of glaucoma; and 2) better determine the appropriate dosage of a particular drug. For example, the expression level of myocilin proteins, alone or in conjunction with the expression level of other genes, known to contribute to glaucoma, can be measured in many patients at various stages of the disease to generate a transcriptional or expression profile of glaucoma. Expression patterns of individual patients can then be compared to the expression profile of glaucoma to determine the appropriate drug and dose to administer to the patient.

The ability to target populations expected to show the highest clinical benefit, based on the GLC1A or glaucoma genetic profile, can enable: 1) the repositioning of marketed drugs with disappointing market results; 2) the rescue of drug candidates whose clinical development has been discontinued as a result of safety or efficacy limitations, which are patient subgroup-specific; and 3) an accelerated and less costly development for

drug candidates and more optimal drug labeling (e.g. since the use of GLC1A as a marker is useful for optimizing effective dose).

These and other methods are described in further detail in the following sections.

5

4.8.1. Prognostic and Diagnostic Assays

The present methods provide means for determining if a subject has (diagnostic) or is at risk of developing (prognostic) glaucoma.

In one embodiment, the method comprises determining whether a subject has
10 an abnormal GLC1A mRNA and/or myocilin protein level, such as by Northern blot analysis, reverse transcription-polymerase chain reaction (RT-PCR), *in situ* hybridization, immunoprecipitation, Western blot hybridization, or immunohistochemistry. According to the method, cells are obtained from a subject and the level of GLC1A mRNA or myocilin level is determined and compared to the mRNA or protein level in a healthy subject. An
15 abnormal level of GLC1A mRNA or myocilin therefor being indicative of an aberrant myocilin bioactivity.

In another embodiment, the method comprises measuring at least one activity of myocilin. Similarly, the constant of affinity of a myocilin protein of a subject with a binding partner can be determined. Comparison of the results obtained with results from
20 similar analysis performed on myocilin proteins from healthy subjects is indicative of whether a subject has an abnormal myocilin activity.

In preferred embodiments, the methods for determining whether a subject has or is at risk for developing glaucoma is characterized as comprising detecting, in a sample of cells from the subject, the presence or absence of a genetic alteration
25 characterized by at least one of (i) an alteration affecting the integrity of a gene encoding a myocilin polypeptide, or (ii) the mis-expression of the GLC1A gene. For example, such genetic alterations can be detected by ascertaining the existence of at least one of (i) a deletion of one or more nucleotides from a GLC1A gene, (ii) an addition of one or more nucleotides to a GLC1A gene, (iii) a substitution of one or more nucleotides of a GLC1A
30 gene, (iv) a gross chromosomal rearrangement of a GLC1A gene, (v) a gross alteration in the level of a messenger RNA transcript of a GLC1A gene, (vi) aberrant modification of a GLC1A gene, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a GLC1A gene, (viii) a non-wild type level of a myocilin polypeptide, (ix) allelic loss of a GLC1A gene, and/or

(x) inappropriate post-translational modification of a myocilin polypeptide. As set out below, the present invention provides a variety of assay techniques for detecting alterations in a GLC1A gene. These methods include, but are not limited to, methods involving sequence analysis, Southern blot hybridization, restriction enzyme site mapping, and methods involving detection of absence of nucleotide pairing between the nucleic acid to be analyzed and a probe. These and other methods are further described *infra*.

Specific diseases or disorders, e.g., genetic diseases or disorders, are associated with specific allelic variants of polymorphic regions of certain genes, which do not necessarily encode a mutated protein. Thus, the presence of a specific allelic variant of a polymorphic region of a gene, such as a single nucleotide polymorphism ("SNP"), in a subject can render the subject susceptible to developing a specific disease or disorder. Polymorphic regions in GLC1A genes, can be identified by determining the nucleotide sequence of genes in populations of individuals. If a polymorphic region, e.g., SNP is identified, then the link with a specific disease can be determined by studying specific populations of individuals, e.g, individuals which developed glaucoma. A polymorphic region can be located in any region of a gene, e.g., exons, in coding or non-coding regions of exons, introns, and promoter region.

It is likely that GLC1A genes comprise polymorphic regions, specific alleles of which may be associated with specific diseases or conditions or with an increased likelihood of developing such diseases or conditions. Thus, the invention provides methods for determining the identity of the allele or allelic variant of a polymorphic region of a GLC1A gene in a subject, to thereby determine whether the subject has or is at risk of developing a disease or disorder associated with a specific allelic variant of a polymorphic region.

In an exemplary embodiment, there is provided a nucleic acid composition comprising a nucleic acid probe including a region of nucleotide sequence which is capable of hybridizing to a sense or antisense sequence of a GLC1A gene or naturally occurring mutants thereof, or 5' or 3' flanking sequences or intronic sequences naturally associated with the subject GLC1A genes or naturally occurring mutants thereof. The nucleic acid of a cell is rendered accessible for hybridization, the probe is contacted with the nucleic acid of the sample, and the hybridization of the probe to the sample nucleic acid is detected. Such techniques can be used to detect alterations or allelic variants at either the genomic or mRNA level, including deletions, substitutions, etc., as well as to determine mRNA transcript levels.

A preferred detection method is allele specific hybridization using probes overlapping the mutation or polymorphic site and having about 5, 10, 20, 25, or 30 nucleotides around the mutation or polymorphic region. In a preferred embodiment of the invention, several probes capable of hybridizing specifically to allelic variants, such as
5 single nucleotide polymorphisms, are attached to a solid phase support, e.g., a "chip". Oligonucleotides can be bound to a solid support by a variety of processes, including lithography. For example a chip can hold up to 250,000 oligonucleotides. Mutation detection analysis using these chips comprising oligonucleotides, also termed "DNA probe arrays" is described e.g., in Cronin et al. (1996) *Human Mutation* 7:244. In one
10 embodiment, a chip comprises all the allelic variants of at least one polymorphic region of a gene. The solid phase support is then contacted with a test nucleic acid and hybridization to the specific probes is detected. Accordingly, the identity of numerous allelic variants of one or more genes can be identified in a simple hybridization experiment.

In certain embodiments, detection of the alteration comprises utilizing the
15 probe/primer in a polymerase chain reaction (PCR) (see, e.g. U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligase chain reaction (LCR) (see, e.g., Landegran et al. (1988) *Science* 241:1077-1080; and Nakazawa et al. (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the GLC1A gene (see Abravaya et al. (1995) *Nuc Acid Res* 23:675-682).
20 In a merely illustrative embodiment, the method includes the steps of (i) collecting a sample of cells from a patient, (ii) isolating nucleic acid (e.g., genomic, mRNA or both) from the cells of the sample, (iii) contacting the nucleic acid sample with one or more primers which specifically hybridize to a GLC1A gene under conditions such that hybridization and amplification of the GLC1A gene (if present) occurs, and (iv) detecting the presence or
25 absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence
30 replication (Guatelli, J.C. et al., 1990, *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh, D.Y. et al., 1989, *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi, P.M. et al., 1988, *Bio/Technology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes

are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In a preferred embodiment of the subject assay, mutations in, or allelic variants, of a GLC1A gene from a sample cell are identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Patent No. 5,498,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the GLC1A gene and detect mutations by comparing the sequence of the sample GLC1A with the corresponding wild-type (control) sequence. Exemplary sequencing reactions include those based on techniques developed by Maxim and Gilbert (*Proc. Natl Acad Sci USA* (1977) 74:560) or Sanger (Sanger et al (1977) *Proc. Nat. Acad. Sci* 74:5463). It is also contemplated that any of a variety of automated sequencing procedures may be utilized when performing the subject assays (*Biotechniques* (1995) 19:448), including sequencing by mass spectrometry (see, for example PCT publication WO 94/16101; Cohen et al. (1996) *Adv Chromatogr* 36:127-162; and Griffin et al. (1993) *Appl Biochem Biotechnol* 38:147-159). It will be evident to one skilled in the art that, for certain embodiments, the occurrence of only one, two or three of the nucleic acid bases need be determined in the sequencing reaction. For instance, A-track or the like, e.g., where only one nucleic acid is detected, can be carried out.

In a further embodiment, protection from cleavage agents (such as a nuclease, hydroxylamine or osmium tetroxide and with piperidine) can be used to detect mismatched bases in RNA/RNA or RNA/DNA or DNA/DNA heteroduplexes (Myers, et al. (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes formed by hybridizing (labelled) RNA or DNA containing the wild-type GLC1A sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent which cleaves single-stranded regions of the duplex as will exist due to base pair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digest the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched

regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton et al (1988) *Proc. Natl Acad Sci USA* 85:4397; Saleeba et al (1992) *Methods Enzymol.* 217:286-295. In a preferred embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in GLC1A cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu et al. (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a GLC1A sequence, e.g., a wild-type GLC1A sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Patent No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations or the identity of the allelic variant of a polymorphic region in GLC1A genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita et al. (1989) *Proc Natl. Acad. Sci USA* 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; and Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments of sample and control GLC1A nucleic acids are denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In a preferred embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen et al. (1991) *Trends Genet* 7:5).

In yet another embodiment, the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE) (Myers et al (1985) *Nature* 313:495). When DGGE

is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing agent gradient to identify differences in the mobility of control and sample DNA (Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753).

Examples of other techniques for detecting point mutations or the identity of the allelic variant of a polymorphic region include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation or nucleotide difference (e.g., in allelic variants) is placed centrally and then hybridized to target DNA under conditions which permit hybridization only if a perfect match is found (Saiki et al. (1986) *Nature* 324:163); Saiki et al (1989) *Proc. Natl Acad. Sci USA* 86:6230). Such allele specific oligonucleotide hybridization techniques may be used to test one mutation or polymorphic region per reaction when oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations or polymorphic regions when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology which depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation or polymorphic region of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs et al (1989) *Nucleic Acids Res.* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238. In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection (Gasparini et al (1992) *Mol. Cell Probes* 6:1). It is anticipated that in certain embodiments amplification may also be performed using Taq ligase for amplification (Barany (1991) *Proc. Natl. Acad. Sci USA* 88:189). In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

In another embodiment, identification of the allelic variant is carried out using an oligonucleotide ligation assay (OLA), as described, e.g., in U.S. Pat. No. 4,998,617 and in Landegren, U. et al., *Science* 241:1077-1080 (1988). The OLA protocol uses two

oligonucleotides which are designed to be capable of hybridizing to abutting sequences of a single strand of a target. One of the oligonucleotides is linked to a separation marker, e.g., biotinylated, and the other is detectably labeled. If the precise complementary sequence is found in a target molecule, the oligonucleotides will hybridize such that their termini abut, and create a ligation substrate. Ligation then permits the labeled oligonucleotide to be recovered using avidin, or another biotin ligand. Nickerson, D. A. et al. have described a nucleic acid detection assay that combines attributes of PCR and OLA (Nickerson, D. A. et al., Proc. Natl. Acad. Sci. (U.S.A.) 87:8923-8927 (1990). In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA.

Several techniques based on this OLA method have been developed and can be used to detect specific allelic variants of a polymorphic region of a GLC1A gene. For example, U.S. Patent No. 5,593,826 discloses an OLA using an oligonucleotide having 3'-amino group and a 5'-phosphorylated oligonucleotide to form a conjugate having a phosphoramidate linkage. In another variation of OLA described in Tobe et al. ((1996) Nucleic Acids Res 24: 3728), OLA combined with PCR permits typing of two alleles in a single microtiter well. By marking each of the allele-specific primers with a unique hapten, i.e. digoxigenin and fluorescein, each OLA reaction can be detected by using hapten specific antibodies that are labeled with different enzyme reporters, alkaline phosphatase or horseradish peroxidase. This system permits the detection of the two alleles using a high throughput format that leads to the production of two different colors.

The invention further provides methods for detecting single nucleotide polymorphisms in a GLC1A gene. Because single nucleotide polymorphisms constitute sites of variation flanked by regions of invariant sequence, their analysis requires no more than the determination of the identity of the single nucleotide present at the site of variation and it is unnecessary to determine a complete gene sequence for each patient. Several methods have been developed to facilitate the analysis of such single nucleotide polymorphisms.

In one embodiment, the single base polymorphism can be detected by using a specialized exonuclease-resistant nucleotide, as disclosed, e.g., in Mundy, C. R. (U.S. Pat. No.4,656,127). According to the method, a primer complementary to the allelic sequence immediately 3' to the polymorphic site is permitted to hybridize to a target molecule obtained from a particular animal or human. If the polymorphic site on the target molecule contains a nucleotide that is complementary to the particular exonuclease-resistant nucleotide derivative present, then that derivative will be incorporated onto the end of the

hybridized primer. Such incorporation renders the primer resistant to exonuclease, and thereby permits its detection. Since the identity of the exonuclease-resistant derivative of the sample is known, a finding that the primer has become resistant to exonucleases reveals that the nucleotide present in the polymorphic site of the target molecule was complementary to that of the nucleotide derivative used in the reaction. This method is advantageous, since it does not require the determination of large amounts of extraneous sequence data.

In another embodiment of the invention, a solution-based method is used for determining the identity of the nucleotide of a polymorphic site. Cohen, D. et al. (French Patent 2,650,840; PCT Appln. No. WO91/02087). As in the Mundy method of U.S. Pat. No. 4,656,127, a primer is employed that is complementary to allelic sequences immediately 3' to a polymorphic site. The method determines the identity of the nucleotide of that site using labeled dideoxynucleotide derivatives, which, if complementary to the nucleotide of the polymorphic site will become incorporated onto the terminus of the primer.

An alternative method, known as Genetic Bit Analysis or GBA™ is described by Goelet, P. et al. (PCT Appln. No. 92/15712). The method of Goelet, P. et al. uses mixtures of labeled terminators and a primer that is complementary to the sequence 3' to a polymorphic site. The labeled terminator that is incorporated is thus determined by, and complementary to, the nucleotide present in the polymorphic site of the target molecule being evaluated. In contrast to the method of Cohen et al. (French Patent 2,650,840; PCT Appln. No. WO91/02087) the method of Goelet, P. et al. is preferably a heterogeneous phase assay, in which the primer or the target molecule is immobilized to a solid phase.

Recently, several primer-guided nucleotide incorporation procedures for assaying polymorphic sites in DNA have been described (Komher, J. S. et al., Nucl. Acids. Res. 17:7779-7784 (1989); Sokolov, B. P., Nucl. Acids Res. 18:3671 (1990); Syvanen, A.-C., et al., Genomics 8:684-692 (1990); Kuppuswamy, M. N. et al., Proc. Natl. Acad. Sci. (U.S.A.) 88:1143-1147 (1991); Prezant, T. R. et al., Hum. Mutat. 1:159-164 (1992); Ugozzoli, L. et al., GATA 9:107-112 (1992); Nyren, P. et al., Anal. Biochem. 208:171-175 (1993)). These methods differ from GBA™ in that they all rely on the incorporation of labeled deoxynucleotides to discriminate between bases at a polymorphic site. In such a format, since the signal is proportional to the number of deoxynucleotides incorporated, polymorphisms that occur in runs of the same nucleotide can result in signals that are

proportional to the length of the run (Syvanen, A. -C., et al., Amer.J. Hum. Genet. 52:46-59 (1993)).

For mutations that produce premature termination of protein translation, the protein truncation test (PTT) offers an efficient diagnostic approach (Roest, et. al., (1993) *Hum. Mol. Genet.* 2:1719-21; van der Lijdt, et. al., (1994) *Genomics* 20:1-4). For PTT, RNA is initially isolated from available tissue and reverse-transcribed, and the segment of interest is amplified by PCR. The products of reverse transcription PCR are then used as a template for nested PCR amplification with a primer that contains an RNA polymerase promoter and a sequence for initiating eukaryotic translation. After amplification of the region of interest, the unique motifs incorporated into the primer permit sequential *in vitro* transcription and translation of the PCR products. Upon sodium dodecyl sulfate-polyacrylamide gel electrophoresis of translation products, the appearance of truncated polypeptides signals the presence of a mutation that causes premature termination of translation. In a variation of this technique, DNA (as opposed to RNA) is used as a PCR template when the target region of interest is derived from a single exon.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid, primer set; and/or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of glaucoma.

Any cell type or tissue may be utilized in the diagnostics described below. In a preferred embodiment a bodily fluid, *e.g.*, blood, is obtained from the subject to determine the presence of a mutation or the identity of the allelic variant of a polymorphic region of a GLC1A gene. A bodily fluid, *e.g.*, blood, can be obtained by known techniques (*e.g.* venipuncture). Alternatively, nucleic acid tests can be performed on dry samples (*e.g.* hair or skin). For prenatal diagnosis, fetal nucleic acid samples can be obtained from maternal blood as described in International Patent Application No. WO91/07660 to Bianchi. Alternatively, amniocytes or chorionic villi may be obtained for performing prenatal testing.

When using RNA or protein to determine the presence of a mutation or of a specific allelic variant of a polymorphic region of a GLC1A gene, the cells or tissues that may be utilized must express the GLC1A gene. Preferred cells for use in these methods include photoreceptors cells of retina. Alternative cells or tissues that can be used, can be identified by determining the expression pattern of the specific GLC1A gene in a subject, such as by Northern blot analysis.

Diagnostic procedures may also be performed *in situ* directly upon tissue sections (fixed and/or frozen) of patient tissue obtained from biopsies or resections, such that no nucleic acid purification is necessary. Nucleic acid reagents may be used as probes and/or primers for such *in situ* procedures (see, for example, Nuovo, G.J., 1992, PCR *in situ* hybridization: protocols and applications, Raven Press, NY).

In addition to methods which focus primarily on the detection of one nucleic acid sequence, profiles may also be assessed in such detection schemes. Fingerprint profiles may be generated, for example, by utilizing a differential display procedure, Northern analysis and/or RT-PCR.

Antibodies directed against wild type or mutant myocilin polypeptides or allelic variants thereof, which are discussed above, may also be used in disease diagnostics and prognostics. Such diagnostic methods, may be used to detect abnormalities in the level of myocilin polypeptide expression, or abnormalities in the structure and/or tissue, cellular, or subcellular location of a myocilin polypeptide. Structural differences may include, for example, differences in the size, electronegativity, or antigenicity of the mutant myocilin polypeptide relative to the normal myocilin polypeptide. Protein from the tissue or cell type to be analyzed may easily be detected or isolated using techniques which are well known to one of skill in the art, including but not limited to western blot analysis. For a detailed explanation of methods for carrying out Western blot analysis, see Sambrook et al, 1989, supra, at Chapter 18. The protein detection and isolation methods employed herein may also be such as those described in Harlow and Lane, for example, (Harlow, E. and Lane, D., 1988, "Antibodies: A Laboratory Manual", Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York), which is incorporated herein by reference in its entirety.

This can be accomplished, for example, by immunofluorescence techniques employing a fluorescently labeled antibody (see below) coupled with light microscopic, flow cytometric, or fluorimetric detection. The antibodies (or fragments thereof) useful in the present invention may, additionally, be employed histologically, as in immunofluorescence or immunoelectron microscopy, for *in situ* detection of myocilin polypeptides. *In situ* detection may be accomplished by removing a histological specimen from a patient, and applying thereto a labeled antibody of the present invention. The antibody (or fragment) is preferably applied by overlaying the labeled antibody (or fragment) onto a biological sample. Through the use of such a procedure, it is possible to determine not only the presence of the myocilin polypeptide, but also its distribution in the examined tissue. Using the present invention, one of ordinary skill will readily perceive

that any of a wide variety of histological methods (such as staining procedures) can be modified in order to achieve such *in situ* detection.

Often a solid phase support or carrier is used as a support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention. The support material may have virtually any possible structural configuration so long as the coupled molecule is capable of binding to an antigen or antibody. Thus, the support configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, test strip, etc. Preferred supports include polystyrene beads. Those skilled in the art will know many other suitable carriers for binding antibody or antigen, or will be able to ascertain the same by use of routine experimentation.

One means for labeling an anti-myocilin polypeptide specific antibody is via linkage to an enzyme and use in an enzyme immunoassay (EIA) (Voller, "The Enzyme Linked Immunosorbent Assay (ELISA)", *Diagnostic Horizons* 2:1-7, 1978, Microbiological Associates Quarterly Publication, Walkersville, MD; Voller, et al., *J. Clin. Pathol.* 31:507-520 (1978); Butler, *Meth. Enzymol.* 73:482-523 (1981); Maggio, (ed.) *Enzyme Immunoassay*, CRC Press, Boca Raton, FL, 1980; Ishikawa, et al., (eds.) *Enzyme Immunoassay*, Kaku Shoin, Tokyo, 1981). The enzyme which is bound to the antibody will react with an appropriate substrate, preferably a chromogenic substrate, in such a manner as to produce a chemical moiety which can be detected, for example, by spectrophotometric, fluorimetric or by visual means. Enzymes which can be used to detectably label the antibody include, but are not limited to, malate dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast alcohol dehydrogenase, alpha-glycerophosphate dehydrogenase, triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase and acetylcholinesterase. The detection can be accomplished by colorimetric methods which employ a chromogenic substrate for the enzyme. Detection may also be accomplished by visual comparison of the extent of enzymatic reaction of a substrate in comparison with similarly prepared standards.

Detection may also be accomplished using any of a variety of other immunoassays. For example, by radioactively labeling the antibodies or antibody fragments, it is possible to detect fingerprint gene wild type or mutant peptides through the use of a radioimmunoassay (RIA) (see, for example, Weintraub, B., *Principles of*
5 *Radioimmunoassays*, Seventh Training Course on Radioligand Assay Techniques, The Endocrine Society, March, 1986, which is incorporated by reference herein). The radioactive isotope can be detected by such means as the use of a gamma counter or a scintillation counter or by autoradiography.

It is also possible to label the antibody with a fluorescent compound. When
10 the fluorescently labeled antibody is exposed to light of the proper wave length, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent labeling compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, α -phthaldehyde and fluorescamine.

The antibody can also be detectably labeled using fluorescence emitting
15 metals such as ^{152}Eu , or others of the lanthanide series. These metals can be attached to the antibody using such metal chelating groups as diethylenetriaminepentaacetic acid (DTPA) or ethylenediaminetetraacetic acid (EDTA).

The antibody also can be detectably labeled by coupling it to a chemiluminescent compound. The presence of the chemiluminescent-tagged antibody is
20 then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isoluminol, thionin acridinium ester, imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound may be used to label the antibody of
25 the present invention. Bioluminescence is a type of chemiluminescence found in biological systems in, which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

Moreover, it will be understood that any of the above methods for detecting
30 alterations in a gene or gene product or polymorphic variants can be used to monitor the course of treatment or therapy.

4.8.2. Pharmacogenomics

Knowledge of the particular alteration or alterations, resulting in defective or deficient GLC1A genes or proteins in an individual (the GLC1A genetic profile), alone or in conjunction with information on other genetic defects contributing to glaucoma (the genetic profile of glaucoma) allows a customization of the therapy for glaucoma to the individual's genetic profile, the goal of "pharmacogenomics". For example, subjects having a specific allele of a GLC1A gene may or may not exhibit symptoms of glaucoma or be predisposed to developing symptoms glaucoma. Further, if those subjects are symptomatic, they may or may not respond to a certain drug, e.g., a specific GLC1A therapeutic, but may respond to another. Thus, generation of a GLC1A genetic profile, (e.g., categorization of alterations in GLC1A genes which are associated with the development of glaucoma), from a population of subjects, who are symptomatic for glaucoma (a glaucoma genetic population profile) and comparison of an individual's GLC1A profile to the population profile, permits the selection or design of drugs that should be safer and more effective for a particular patient or patient population (i.e., a group of patients having the same genetic alteration).

For example, a GLC1A population profile can be performed, by determining the GLC1A profile, e.g., the identity of GLC1A genes, in a patient population having glaucoma. Optionally, the GLC1A population profile can further include information relating to the response of the population to a GLC1A therapeutic, using any of a variety of methods, including, monitoring: 1) the severity of symptoms associated with the GLC1A related disease, 2) GLC1A gene expression level, 3) GLC1A mRNA level, and/or 4) GLC1A protein level. and (iii) dividing or categorizing the population based on the particular genetic alteration or alterations present in its GLC1A gene or a GLC1A pathway gene. The GLC1A genetic population profile can also, optionally, indicate those particular alterations in which the patient was either responsive or non-responsive to a particular therapeutic. This information or population profile, is then useful for predicting which individuals should respond to particular drugs, based on their individual GLC1A profile.

In a preferred embodiment, the GLC1A profile is a transcriptional or expression level profile and step (i) is comprised of determining the expression level of GLC1A proteins, alone or in conjunction with the expression level of other genes, known to contribute to the same disease. The GLC1A profile can be measured in many patients at various stages of the disease.

Pharmacogenomic studies can also be performed using transgenic animals. For example, one can produce transgenic mice, e.g., as described herein, which contain a specific allelic variant of a GLC1A gene. These mice can be created, e.g, by replacing their wild-type GLC1A gene with an allele of the human GLC1A gene. The response of these mice to specific GLC1A therapeutics can then be determined.

4.8.3. Monitoring of Effects of GLC1A Therapeutics During Clinical Trials

The ability to target populations expected to show the highest clinical benefit, based on the GLC1A or disease genetic profile, can enable: 1) the repositioning of marketed drugs with disappointing market results; 2) the rescue of drug candidates whose clinical development has been discontinued as a result of safety or efficacy limitations, which are patient subgroup-specific; and 3) an accelerated and less costly development for drug candidates and more optimal drug labeling (e.g. since the use of GLC1A as a marker is useful for optimizing effective dose).

The treatment of an individual with a GLC1A therapeutic can be monitored by determining GLC1A characteristics, such as myocilin protein level or activity, GLC1A mRNA level, and/or transcriptional level. This measurements will indicate whether the treatment is effective or whether it should be adjusted or optimized. Thus, GLC1A can be used as a marker for the efficacy of a drug during clinical trials.

In a preferred embodiment, the present invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate, for example a drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a preadministration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of a myocilin protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression or activity of the myocilin protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the myocilin protein, mRNA, or genomic DNA in the preadministration sample with the myocilin protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression of a wildtype GLC1A gene or activity of a wildtype myocilin protein to higher levels than detected. Alternatively, decreased administration of

the agent may be desirable to decrease expression of a mutant GLC1A gene or activity of a mutant myocilin protein to lower levels than detected.

Cells of a subject may also be obtained before and after administration of a GLC1A therapeutic to detect the level of expression of genes other than GLC1A, to verify that the GLC1A therapeutic does not increase or decrease the expression of genes which could be deleterious. This can be done, e.g., by using the method of transcriptional profiling. Thus, mRNA from cells exposed in vivo to a GLC1A therapeutic and mRNA from the same type of cells that were not exposed to the GLC1A therapeutic could be reverse transcribed and hybridized to a chip containing DNA from numerous genes, to thereby compare the expression of genes in cells treated and not treated with a GLC1A therapeutic. If, for example a GLC1A therapeutic turns on the expression of a proto-oncogene in an individual, use of this particular GLC1A therapeutic may be undesirable.

The present invention is further illustrated by the following examples which should not be construed as limiting in any way. The contents of all cited references (including literature references, issued patents, published patent applications as cited throughout this application are hereby expressly incorporated by reference. The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See, for example, *Molecular Cloning A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989); *DNA Cloning*, Volumes I and II (D. N. Glover ed., 1985); *Oligonucleotide Synthesis* (M. J. Gait ed., 1984); Mullis et al. U.S. Patent No: 4,683,195; *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*, Vols. 154 and 155 (Wu et al. eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

The present invention is further illustrated by the following examples which should not be construed as limiting in any way. The contents of all cited references (including literature references, issued patents, published patent applications, and co-pending patent applications) cited throughout this application are hereby expressly incorporated by reference.

5. 1 Genetic Linkage of Familial Open Angle Glaucoma to Chromosome 1q21-q31

Materials and Methods

Pedigree

A family in which five consecutive generations have been affected with juvenile-onset, open-angle glaucoma without iridocorneal angle abnormalities was identified. The family comprised descendants of a woman who emigrated from Germany to the midwestern United States in the late 1800s. The disease state in affected family members included onset during the first 3 decades of life, normal anterior chamber angles, high intraocular pressures, lack of systemic or other ocular abnormalities, and need for surgery to control the glaucoma in affected individuals. A total of 35 family members at 50% risk for glaucoma had complete eye examinations including visual acuity with refraction, slit-lamp biomicroscopy, applanation tomometry, gonioscopy, stereo disc photography and Humphrey, Goldmann or Octopus perimetry. Two other affected patients were ascertained by reviewing records of other ophthalmologists. Patients were considered to be affected for linkage if they had documented pressures greater than 30 mm Hg and evidence of optic nerve or visual field damage; or, if they had intraocular pressures greater than 22 mm Hg and an obviously affected child. Affected family members are characterized by an early age of diagnosis, a normal appearing trabecular meshwork, very high intraocular pressures (often above 50 mm Hg), and relatively pressure-resistant optic nerves. Figure 1 is a pictorial representation of the pedigree.

DNA typing

Blood samples were obtained from all living affected family members as well as six spouses of affected patients with children. 10ml blood were obtained from each patient in EDTA-containing glass tubes. DNA was prepared from the blood using a non-organic extraction procedure (Grimberg, J. et al. Nucl. Acids Res 17, 8390 (1989)). Short tandem repeat polymorphisms (STRPs) distributed across the entire autosomal genome were selected from the literature or from those kindly provided by J.L. Weber. The majority were [dC-dA]-[dG-dT] dinucleotide repeats. Oligonucleotide primers flanking each STRP were synthesized using standard phosphoramidite chemistry (Applied Biosystems model 391 DNA synthesizer). Amplification of each STRP was performed with 50 ng. of each patient's DNA in a 8.35 l PCR containing each of the following: 1.25 l 10 X buffer (100mM Tris-HCl pH 8.8, 500 mM KCl, 15 mM MgCl₂, 0.01% w/v gelatin), 300 M each of dCTP, dGTP and dTTP, 37M dATP, 50pmoles each primer, 0.25 l -³⁵S-dATP (Amersham, >1000 Ci mmol⁻¹), and 0.25 U *Taq* polymerase (Perkin-Elmer/Cetus). Samples were incubated in a DNA thermocycler (Perkin-Elmer/Cetus) for 35 cycles under the following conditions: 94C for 30 s, 55C for 30 s, and 72C for 30 s. Following amplification, 5l of stop solution (95% formamide, 10mM NaOH, 0.05% Bromophenol Blue, 0.05% Xylene Cyanol) was added to each sample. Following denaturation for 3 min at 95C, 5 l of each sample was immediately loaded onto prewarmed polyacrylamide gels (6% polyacrylamide, 7 M urea) and electrophoresed for 3-4h. Gels were then placed on Whatman, 3mm paper and dried in a slab gel dryer. Autoradiographs were created by exposing Kodak Xomat AR film to the dried gels for 24-36h.

Linkage analysis

Genotypic data from the autoradiographs were entered into a Macintosh computer. A Hypercard-based program (Nichols, BE et al., Am J Hum Genet 51 A369 (1992)) was used to store and retrieve marker data as well as to export it to a DOS-compatible machine for analysis with the computer program LINKAGE (version 5.1) (Lathrop, GM and LaLouel, JM 359, 794-801 (1992)). Allele frequencies were assumed to be equal for each marker. The MLINK routine was used for pairwise analysis. The relative odds of all possible orders of the disease and two markers (D1S191 and D1S194) was performed under the ILINK program. Significance of linkage was evaluated using the standard criterion ($Z_{\max} > 3.0$).

Results

clinical findings

All of the 37 family members studied were at 50% risk of having the disease because of a known affected parent or sibling. Nineteen of these patients had elevated intraocular pressures and visual field defects consistent with the diagnosis of primary open angle glaucoma. Three more patients had moderately elevated intraocular pressures and obviously affected children.

linkage analysis

Over 90 short tandem repeat polymorphisms were typed the family before linkage was detected with markers that map to the long arm of chromosome 1. Two-point maximum likelihood calculations using all available family members and 33 chromosome 1 markers revealed significant linkage to eight of them (Table 2). D1S212 was fully informative for all affected members of the family, and pairwise linkage analysis produced a lod score of 6.5 ($= 0$). Multipoint linkage analysis did not add to the peak lod score. The glaucoma locus was therefore determined to be located in a region of about 20 centiMorgans (cM) in size between D1S191 and D1S194. Both of these markers demonstrated multiple recombinants (two and three, respectively) in affected individuals in the family. The order D1S191-glaucoma-D1S194 was more than 1,000 times more likely than the other two possible orders.

Table 6 Pairwise linkage data

		Recombination Fraction									
		0.15	0.20	0.25	0.30	0.40	Z_{ma}	Locu		$\hat{\theta}$	
								x	s		
25	D1S212	6.0	5.4	4.8	4.2	3.6	2.9	1.4	6.5	0.00	1
	D1S215	5.1	4.6	4.0	3.5	2.9	2.3	1.0	5.6	0.00	1
	D1S218	4.7	4.3	3.8	3.3	2.7	2.2	1.0	5.2	0.00	1
	D1S238	4.4	4.2	3.9	3.4	2.9	2.4	1.2	4.4	0.04	1
	D1S117	3.8	3.6	3.3	2.8	2.3	1.8	0.7	3.8	0.04	1q
30	D1S104	3.2	2.9	2.6	2.3	2.0	1.6	0.7	3.4	0.00	1q21-q23
	D1S191	3.0	3.2	3.0	2.7	2.4	1.9	0.9	3.2	0.09	1
	D1S196	2.9	2.6	2.3	2.0	1.6	1.3	0.5	3.1	0.00	1

Table 6 Pairwise linkage data

Recombination fraction

0.05 0.19

5 5.2 Genetic Fine Mapping of the Juvenile Primary Open Angle
Glaucoma Locus and Identification and Characterization of a Glaucoma
Gene

Once primary linkage has been identified, the next step in identifying any disease gene by positional cloning is the narrowing of the candidate locus to the smallest possible genetic region. The initial study described in Example 5.1 demonstrated that a
10 primary open angle glaucoma gene lies within an approximately 20 cM region flanked by markers D1S194 and D1S191 on chromosome 1q. Additional markers and families were obtained and used to refine the genetic locus to a 2.5 cM region using two of these families. The third family should allow the interval to be further narrowed.

15 In addition to the family resources, polymorphic DNA markers and genetic maps were used to refine the 1q glaucoma locus. Using STRPs, the genotype of each family member was determined. Amplification of each STRP was performed using the following protocol:

20 1) Dilute genomic DNA (about 1g/l) 1/50 i.e. 20l "stock" DNA and 980 dd H₂O.

2) Use 2.5l of "dilute" DNA as template for PCR

3) Prepare PCR reaction mix as follows:

25 1.25l 10 X Buffer (Stratagene)
0.12l of each primer (50pmoles each primer)
0.5l dNTPs (5mM C,T,&G and 0.625 mM A "cold")
3.5l dd H₂O
0.25l ³⁵S-dATP
30 0.1l Taq polymerase
oil (one drop)

4) Perform PCR at optimal conditions for given primers (usually 94 30 s, 55 30s and 72 30 s) and run for 35 cycles.

5) Add 5l stop solution (95% formamide, 10mM NaOH, 0.05% bromophenol blue, 0.05% xylene cyanol) to each tube.

5 6) Denature samples at 95C for 3 minutes and load immediately onto a prewarmed polyacrylamide gel.

7) Dry gels on Whatmann paper and expose autoradiography film for 1-2 days.

10 Where possible, multiple loadings of different STRPs on gels were performed. Up to 6 markers per gel have been successfully loaded. In addition, the PCR amplification (up to three markers) have been successfully multiplexed. The juvenile glaucoma gene is believed to lie between markers AFM238 and AT3 (an 8 centimorgan interval) based on observed recombinations within the families studied. Haplotypic analysis between families has further narrowed this interval to the 2 centimorgan interval between D1S210 and AT3.

15 Since the genetic interval has been narrowed significantly physical mapping strategies can be used. The closest flanking markers to screen total human genomic yeast artificial chromosome (YAC) libraries to identify YACs mapping to the region of interest. The CEPH and CEPH mega-YAC libraries can be used for this purpose (available from the Centre d'Etude du Polymorphisme Humain (CEPH) Paris, France). Forty-four percent of the clones in the CEPH mega-YAC library have an average size of 560 kb, an additional 21% have an average size of 800 kb, and 35% have an average size of 120 kb. This library is available in a gridded micro-titer plate format such that only 50-200 PCR reactions need to be performed using a specific sequence tagged site (STS) to identify a unique YAC containing the STS. The YAC contigs identified by CEPH have been used to begin constructing a contig across the 1q candidate region (see Figure 3). YAC contigs using YAC ends can be constructed to identify additional YACs. YAC ends can be rescued using anchored PCR (Riley, J. et al (1990) *Nucleic Acids Res* 18:2887-2890), the ends can then be sequenced and the sequence can be used to develop a sequence tagged site (STS). The STS can be used to rescreen the YAC library to obtain an overlapping adjacent YAC.

Because some YACs have been shown to be chimeric or to contain deletions or rearrangements, particularly those from the mega YAC library, the correctness of each YAC contig should be verified by constructing a pulse field map of the region. In addition, chimeric YACs are minimized by ensuring that the YAC maps to a single chromosome by fluorescent in situ hybridization (FISH) or that the two YAC ends map to the same chromosome using monochromosomal somatic cell hybrids (NIGMs Panel 2). In addition, the YAC chimera problem can be minimized by not relying on any single YAC to span a given chromosome segment, but rather by obtaining at least two overlapping independent YACs to ensure coverage of a given region.

Once a YAC contig spanning the candidate region has been isolated, this reagent can be used to generate additional genetic markers for potentially finer genetic mapping. In addition, the YACs can be used to make higher resolution physical mapping reagents such as region specific lambda and cosmid clones. Lambda and cosmid clones can be used for isolation of candidate genes. A modification of "exon trapping" (Duyk, G.M. (1990) *Proc Natl Acad Sci USA* 87:8995-8999) known as exon amplification (Buckler, A.J. (1991) *Proc Natl Acad Sci USA* 88:4005-4009) can be used to identify exons from genes within the region. Exons trapped from the candidate region can be used as probes to screen eye cDNA libraries to isolate cDNAs. Where necessary, other strategies can be utilized to identify genes in genomic DNA including screening cDNA libraries with YAC fragments subcloned into cosmids, zoo blot analysis, coincidence cloning strategies such as direct selection of cDNAs with biotin-streptavidin tagged cosmid clones (Morgan, J.G. et al (1992) *Nucleic Acid Res* 20 (19):5173-5179), and HTF island analysis (Bird, A.P. (1987) *Trends Genet* 3:342-247). Promising genes will be further evaluated by searching for mutations using GC-clamped denaturing gradient gel electrophoresis (Sheffield, V.C. et al (1989) *Genomics* 16:325-332), single strand conformational gel polymorphism (SSCP) analysis (Orita, M. et al (1989) *Proc Natl Acad Sci USA* 86:2766-2770) and direct DNA sequencing.

5.3 Primer Pairs for Use In Identifying Subjects Having a Predisposition to Glaucoma

Two primer pairs that can be used in conjunction with the polymerase chain reaction to amplify a 190 base pair sequence from human genomic DNA that harbors mutations causing glaucoma (primers 1 and 2 in Table 7) have been identified.

TABLE 7

Primer 1	forward - ATACTGCCTAGGCCACTGGA (SEQ ID NO. 12) reverse - CAATGTCCGTGTAGCCACC (SEQ ID NO. 13)
Primer 2	forward - GAACTCGAACAAACCTGGGA (SEQ ID NO. 14) reverse - CATGCTGCTGTACTTATAGCGG (SEQ ID NO. 15)

These primers were used to screen 410 patients with glaucoma and 81 normal individuals. Four amino acid altering sequence changes were detected in a total of 12 glaucoma patients (2.9%). No amino acid altering sequence changes were observed in the normal individuals.

The prevalence of mutations in the segment of DNA amplified by these primer pairs suggest that use of these primers in conjunction with an appropriate detection method can be used to identify a predisposition to glaucoma in approximately 100 thousand patients in the United States alone.

5.4 Additional Primer Pairs and Their Use In Identifying Subjects Having a Predisposition to Glaucoma

The study was approved by the Human Subjects Review Committee at the University of Iowa and informed consent was obtained from all study participants. Primary open angle glaucoma was defined as the presence of an intraocular pressure over 21 mm Hg as well as evidence of glaucomatous optic nerve head damage. Visible optic nerve head damage alone was accepted if there was documented enlargement of the optic nerve head cup. Otherwise, both a large optic nerve head cup with a thin neural rim and characteristic optic nerve related visual field loss were required. Patients were excluded if they had a history of eye surgery prior to the diagnosis of glaucoma or evidence of secondary glaucoma, such as exfoliation or pigment dispersion. Normal volunteers were over 40 years of age, had intraocular pressures under 20 mm Hg, and had no family or personal history of glaucoma. 716 unrelated patients affected with primary open angle glaucoma (POAG) and 91 volunteers were screened for mutations in the coding sequence of the GLC1A gene. This was accomplished with an electrophoretic procedure known as single strand conformation polymorphism analysis

(SSCP). The sequences of the oligonucleotide primers used for the GLC1A assay are presented in Table 8.

Table 8			
Primer Pairs			
	Exon	Forward Primer	Reverse Primer
5	1	SEQ ID No. 16	SEQ ID No. 17
	1	SEQ ID No. 18	SEQ ID No. 19
	1	SEQ ID No. 20	SEQ ID No. 21
	1	SEQ ID No. 22	SEQ ID No. 23
	1	SEQ ID No. 24	SEQ ID No. 25
	1	SEQ ID No. 26	SEQ ID No. 27
10	2	SEQ ID No. 28	SEQ ID No. 29
	3	SEQ ID No. 30	SEQ ID No. 31
	3	SEQ ID No. 32	SEQ ID No. 33
	3	SEQ ID No. 34	SEQ ID No. 35
	3	SEQ ID No. 36	SEQ ID No. 37
	3	SEQ ID No. 38	SEQ ID No. 39
15	3	SEQ ID No. 40	SEQ ID No. 41
	3	SEQ ID No. 40	SEQ ID No. 41

Mutations were confirmed with automated DNA sequencing. 227 of the patients (32%) were ascertained because of a positive family history of glaucoma while 402 (56%) were ascertained consecutively in a single glaucoma clinic (the University of Iowa). Overall, 563 of the patients were ascertained in Iowa, 97 in Australia and the remainder from elsewhere in the United States. All of the normal volunteers were collected in Iowa. More than 75% of the patients in each group were Caucasian. A portion of the GLC1A gene had been previously evaluated for mutations in 330 of these same glaucoma patients and all 91 normal volunteers (see above). However, in this study, the entire coding region was evaluated. An additional 505 unrelated control individuals with an unknown glaucoma status were also evaluated for sequence changes. Three hundred and eighty of these control patients had been previously screened for mutations in a portion of exon 3. 184 of these general population controls were connected in Iowa and 13 in Australia. Family members of the probands found to

harbor GLC1A sequence changes were also evaluated for mutations. Efforts were made to examine or review the medical records of all molecularly affected family members. The age of onset and the highest recorded intraocular pressures were associated with six different mutations were evaluated with a Kruskal-Wallis non-parametric analysis of variance. All p values were two-tailed. In the four largest families, co-segregation of a GLC1A mutation and the disease phenotype was evaluated with the LOD score method as described above

5.5 Cloning and Sequencing Human and Mouse GLC1A and Northern Blot Analysis of Expression

BAC screening. BAC clones containing the human GLC1A gene were identified by screening human BAC library pools (Research Genetics, Huntsville, AL) with a PCR-based assay. One microliter of BAC pool DNA was used as template in an 8.35 μ l PCR reaction containing 1.25 μ l of 10X buffer (100 mM tris-HCl, pH 8.3, 500 mM KCl, 15 mM MgCl₂); deoxynucleotides dCTP, dATP, dTTP, and dGTP (300 μ M each); 1 pmol of each primer; and 0.25 units of *Taq* polymerase (Boehringer Mannheim, Indianapolis, IN). The primers used in the screening assay were specific for exon three of GLC1A (FWD: 5' ATACTGCCTAGGCCACTGGA 3' (SEQ ID No. 34) and REV: 5' CAATGTCCGTGTAGCCACC 3' (SEQ ID No. 35)). Samples were denatured at 94°C for 5 minutes and incubated for 35 cycles at 94°C 30s, 55°C 30s, 72°C 30s in a DNA thermocycler (Omnigene, Teddington, Middlesex, UK). After amplification, 5 μ l of stop solution (95% formamide, 10 mM NaOH, 0.5% bromophenyl blue, 0.05% xylene cyanol) were added. Amplification products were electrophoresed on 6% polyacrylamide-5% glycerol gels at 50 W for approximately 2 hours. After electrophoresis, gels were stained with silver nitrate (Bassam 1991). A BAC containing the mouse GLC1A orthologue was identified by screening the mouse 129 BAC library pools (Research Genetics, Huntsville AL). Primers specific for exon three of the human GLC1A gene (FWD: 5' TGGCTACCACGGACAGTTC 3' (SEQ ID No. 36) and REV: 5' CATTGGCCACTGACTGCTTA 3' (SEQ ID No. 37) were used for a primary PCR-based screen as described above. The primary screen identified sub-pools of BACs which contained the mouse GLC1A gene. Filters blotted with the BACs in the subpools (Research Genetics, Huntsville, AL) were screened by hybridization with a digoxigenin probe using the Genius System hybridization kit (Boehringer Mannheim, Indianapolis, IN). Digoxigenin labeled probe for hybridization was generated by PCR amplifying 50

ng of mouse 129 DNA in a 25 μ l reaction containing 3.75 μ l of 10X buffer; 1.5 μ l of labeling dNTP mixture (1 mM dATP, 1 mM dCTP, 1mM dGTP 0.65 mM dTTP, and 0.35 mM of digoxigenin conjugated dUTP); 7.6 pmoles each of FWD and REV primer; and 1.25 units of Taq polymerase (Boehringer Mannheim, Indianapolis, IN). PCR reaction conditions were as described above. Hybridization conditions were as recommended by the manufacturer.

The human GLCIA cDNA sequence was used to select PCR primers that produced an amplification product of identical size when using both human and mouse genomic DNA as template. The amplification products were sequenced to confirm that they were from the human GLCIA gene and the mouse orthologue of this gene. The PCR primers were then used to screen both a human and mouse BAC library. Both human and mouse BACs containing the GLCIA gene were identified, subcloned into plasmids, and several clones covering each GLCIA gene were identified. These subclones were used to generate both human and mouse genomic GLCIA sequence.

Subcloning. The mouse and human BACs containing the GLCIA gene were digested with either EcoR1, Aval, Acc1, or BamH1 and ligated into either pT7-blue (Novagen, Milwaukee, WI) or pUC19.

Sequencing. PCR products and BAC subclones were sequenced with fluorescent dideoxynucleotides on an Applied Biosystems (ABI) model 373 or 377 automated sequencer.

GLCIA CA repeat polymorphisms. The CA repeat polymorphism upstream of the GLCIA gene was PCR amplified with primers 5'-TTCCTTCAGGTTGGGAGATG-3' (SEQ ID No. 42) and 5'-GAGAGCACCAGGAGATGGAG-3' (SEQ ID No. 43). The PCR reaction conditions were as described in the BAC screening section. Allele frequencies for the upstream polymorphism are: Allele 1, 1.1%; Allele 2, 2.2%; Allele 3, 48.9%; Allele 4, 1.1%; Allele 5, 21.1%; Allele 6, 25.6%. Allele frequencies for the downstream polymorphism are: Allele 1, 25.3%; Allele 2, 13%, Allele 3, 60.3%, Allele 4, 1.4%.

Sequence comparison. DNA sequences were aligned and contigs were formed using the Sequencher DNA analysis package (DNA Codes, Ann Arbor, MI). Putative enhancer and promoter elements were identified using the internet resource TESS (<http://agave.humgen.upenn.edu/utess/>) and the transcription factor binding site data set TRANSFAC v3.2. The predicted protein sequence was analyzed with PROSITE, Tmpred, NetOgly, and SignalP software packages available on the internet at

<http://expasy.hcuge.chsprot/prosite.html>;
http://ulrec3.unil.ch/software/TMPED_form.html;
<http://genome.cbs.dtu.dk/services/netOGLYC/>;

- 5 <http://www.cbs.dtu.dk/services/SignalP/>. Data base searches for expression of the GLCIA gene used the program BLAST and the data bases dbest and NR available on the internet at <http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-blast?Jform=0>.

10 *Northern blot analysis.* Human Multiple Tissue Northern (MTN) blots (Clontech, San Francisco, CA) were probed either with the entire human GLCIA cDNA sequence or with a section of exon three of the human GLCIA gene corresponding to codon 315 to the termination site. The probes were labeled with ³²P-(dCTP) using Ready-To-Go DNA Labeling Beads (-dCTP) (Pharmacia Biotech, Piscataway, NJ). Hybridization was for 16 hours at 42°C in 50% formamide, 5X standard saline citrate (5X SSC: 0.75M sodium chloride, 0.075M sodium acetate), 1X Denhardt's solution, 20mM phosphate buffer (pH 7.5), 1% sodium dodecyl sulfate (SDS), 100 µg/ml salmon
15 sperm DNA, and 10% dextran sulfate. Following hybridization, blots were washed twice at room temperature in 1X SSC, rinsed twice in 1X SSC / 1% SDS at 65°C , and washed once in 0.1X SSC, 0.1% SDS to confirm the specificity of the hybridization. Autoradiography was performed with Kodak XAR-5 film at -70°C with DuPont Cronex
20 Lightning Plus intensifying screens (DuPont, Wilmington, DE).

Claims

1. An isolated nucleic acid molecule comprising a nucleic acid molecule or the
5 complement of a nucleic acid molecule set forth in any of SEQ ID Nos. 16, 17, 18, 19,
20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42 or
43.
2. An isolated nucleic acid molecule comprising a nucleic acid molecule or the
10 complement of a nucleic acid molecule obtained by amplifying a GLC1A gene with a
primer pair selected from the group consisting of SEQ ID Nos 16 and 17, SEQ ID Nos
18 and 19, SEQ ID Nos 20 and 21, SEQ ID Nos 22 and 23, SEQ ID Nos 24 and 25, SEQ
ID Nos 26 and 27, SEQ ID Nos 28 and 29, SEQ ID Nos 30 and 31, SEQ ID Nos 32 and
33, SEQ ID Nos 34 and 35, SEQ ID Nos 36 and 37, SEQ ID Nos 38 and 39, SEQ ID
15 Nos 40 and 41, SEQ ID Nos 42 and 43.
3. An isolated nucleic acid molecule of claim 2, which appears within Exon 1 of Figure
1 or is the complement of a a nucleic acid molecule, which appears within Exon 1.
- 20 4. An isolated nucleic acid molecule of claim 2, which appears within Exon 2 of Figure
1 or is the complement of a a nucleic acid molecule, which appears within Exon 2.
5. An isolated nucleic acid molecule of claim 2, which appears within Exon 3 of Figure
1 or is the complement of a a nucleic acid molecule, which appears within Exon 3.
25
6. An isolated nucleic acid of claim 3, wherein the primer pair is comprised of a
member selected from the group consisting of: SEQ ID Nos. 16 and 17; SEQ ID Nos.18
and 19; SEQ ID Nos. 20 and 21; SEQ ID Nos. 22 and 23; SEQ ID Nos. 24 and 25; and
SEQ ID Nos. 26 and 27..
30
7. An isolated nucleic acid of claim 4, wherein the primer pair is comprised of SEQ ID
Nos. 28 and 29.

8. An isolated nucleic acid of claim 5, wherein the primer pair is comprised of SEQ ID Nos 30 and 31, SEQ ID Nos 32 and 33, SEQ ID Nos 34 and 35, SEQ ID Nos 36 and 37, SEQ ID Nos 38 and 39, SEQ ID Nos 40 and 41.
- 5 9. An isolated nucleic acid of claim 2, which is upstream of the GLC1A gene and is amplified by SEQ ID Nos 42 and 43.
10. A method for determining whether a subject has or has the potential for developing primary open angle glaucoma, comprising the steps of:
- 10 a) obtaining a biological sample containing genomic DNA or a complement thereof from a subject;
- b) performing an amplification on the genomic DNA using a primer pair selected from the group consisting of SEQ ID Nos 16 and 17, SEQ ID Nos 18 and 19, SEQ ID Nos 20 and 21, SEQ ID Nos 22 and 23, SEQ ID Nos 24 and 25, SEQ ID Nos 26 and 27, SEQ ID Nos 28 and 29, SEQ ID Nos 30 and 31, SEQ ID Nos 32 and 33, SEQ ID Nos 34 and 35, SEQ ID Nos 36 and 37, SEQ ID Nos 38 and 39, SEQ ID Nos 40 and 41, SEQ ID Nos 42 and 43, thereby obtaining an amplification product; and
- 15 c) analyzing the amplification product for the presence of a mutation, wherein the presence of a mutation indicates that the subject has or has
- 20 the potential for developing primary open angle glaucoma.
- 25 11. A screening method of claim 10, wherein in step c), the amplification product is analyzed using single strand conformation polymorphism (SSCP) analysis.
12. A screening method of claim 10, wherein in step c), the amplification product is analyzed by sequencing.
- 30

13. A kit for diagnosing a subject as having primary open angle glaucoma comprising:

a) a primer pair selected from the group consisting of: SEQ ID Nos 16 and 17, SEQ ID Nos 18 and 19, SEQ ID Nos 20 and 21, SEQ ID Nos 22 and 23, SEQ ID Nos 24 and 25, SEQ ID Nos 26 and 27, SEQ ID Nos 28 and 29, SEQ ID Nos 30 and 31, SEQ ID Nos 32 and 33, SEQ ID Nos 34 and 35, SEQ ID Nos 36 and 37, SEQ ID Nos 38 and 39, SEQ ID Nos 40 and 41, SEQ ID Nos 42 and 43.; and

b) instructions for using the primer pair to perform an amplification.

5
10

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Exon 1

huGLC1A	agcgcaggaggagagaagagaggggtagtgtagcaagaagaagacagattcattcaagggcagtggaattgaccacagggattatagtcacag	GR
moGLC1A	tacctggtagtctgttggctggccaatctaaccaaatcagtgatcccccaagctcagcgagacaatccgtctcaaaaaaacaagaaggagagaatgaagaaga	GR
huGLC1A	tgatcctgggttctaggaggcagggtatattgtggggggaaaaaatcagttcaagggaagtcgggagacgtgatttctaatactatatattttccttttac	GR
moGLC1A	caacgctgacataagcctctagctcacacacacacacacacagcctatacacatgagtggtgcacccaccaggtgaacgcagatgcacacatac	
huGLC1A	aagctgagtaattctgagcaagtcacaaggtagtaactgaggtgtaagattacttagtttctccttattagggaactcttttctctgtggagttagcag	GR
moGLC1A	ccccccacacaagaatggatttagagcaaggcacttgctcagtccttcaggcgaatctgctatgggaaacatcagagaaattttatcacacagatatcac	GR
huGLC1A	cacaagggcaatcccgttctttaaacagggaagaaaaacattcctaagagtaaaagccaaacagattcaagcctaggctcttgctgactatatgattggtttt	
moGLC1A	aaatgctattattagtagtctgagaaccaagttgctcaaatgcaaatgttgctctaaaggaacccatgagggggcagtgaggtggctgagagggggagggtgc	
huGLC1A	ttgaaaaaatcatttcaggcatgtttactatctgattcagaaaaatgagactagtagtaccctttggtcagctgtaaacaaacacccatttgtaaatgtctcaag	
moGLC1A	ttagtgagcaggccttacagactgaggtcagtccttaagcccatgcccaggaggagagaactggacccccaaaagtgtgctctctgaccacacacggcatg	GR
huGLC1A	ttcagggttaactgcagaaccaatcaaaataagaatagaatcttttagagaaactgtgtttctccactctggagggtgagctgccaggggcagtttggaat	GR
moGLC1A	catggcccatgtgtgctcatatcccccccatatgagcacacaccagtaagtaaacatttataaagatgttccatgaggttccacgcacacacacggcttat	

Fig. 1A-1

[illegible]

Fig. 1A-3

Fig. 1A-4

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huGLC1A
CCAGAGCAAGGtaagaatgcagagtgaggggactctgagttcagcaggtgatggctgtagtgacctgctacaggcgctccaggcctccctgacctgcc
**** **

moGLC1A
CCAGGCAAGGtaagagtgagggtggagtgccacctgacccagaaaggtagcaagtttgctggtgacccattacaggacccccagggttctccttctgtt

huGLC1A
tttctctagagactgcacagctagcacagacagatgaattaaaggaaagcacagcgtacaccttcaggtattactagtaatttagctccttgagagcttc
moGLC1A
ttgtctttctcagaaactgcaatccagcatgcagtgtttcattaaggagagagaaagcaaaccttttgcatgcttctagaaagttggctccttgt

at t t a g a t t a g t g g t t c a g a g t t c t t g t g c c c c t c c a t g t c a g t t t t c a c a g t c c a t a g c a a a g g a g a a t a a a a g g a c c g g g t g a g a t g t g t c t c g a t
t t a g g t c a g t g g a t c t g a g c t c t t g t g c c a g t c a t g a c a a a t g a t c a t g g c c a c a g c c a a a t g a c a a a c a t g g g g c c a g g t g g c a g a t a c a t a t g a t

Fig. 1A-5

[illegible]

Fig. 1B

SUBSTITUTE SHEET (RULE 26)

[illegible]

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[illegible]

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Fig. 1C-3

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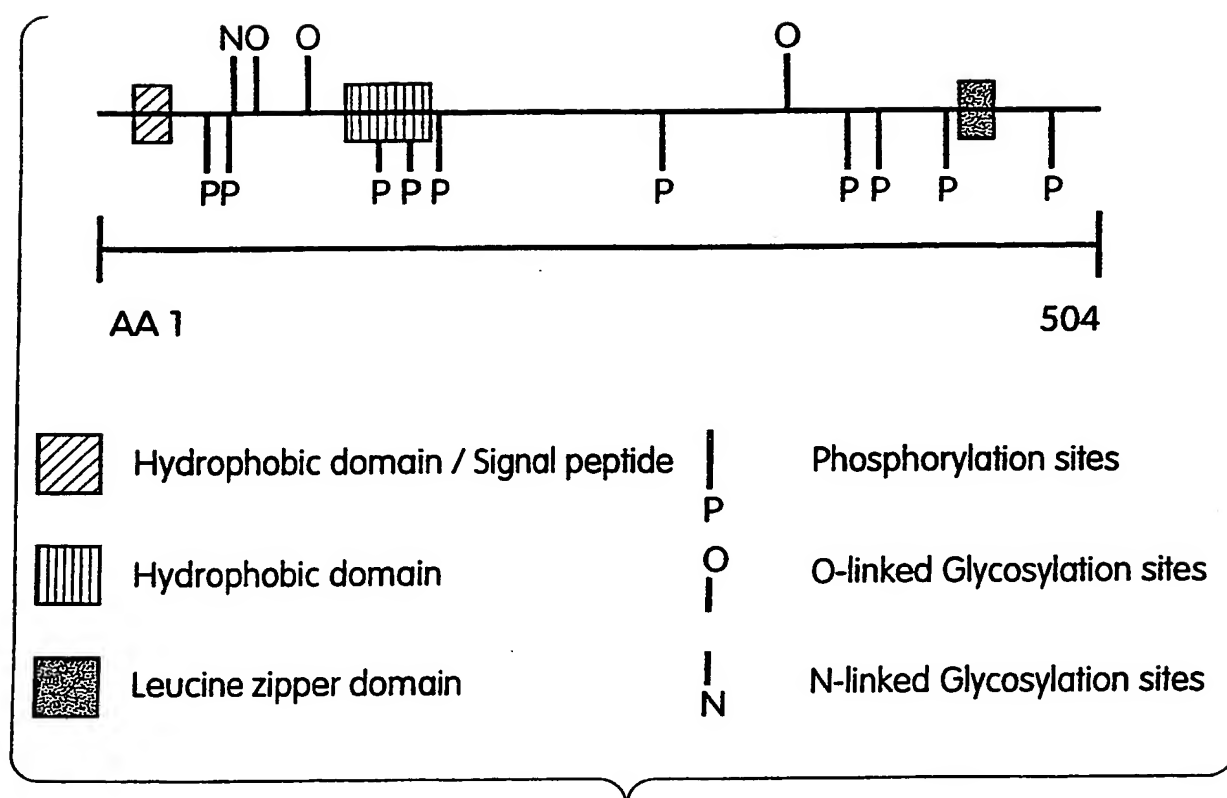


Fig. 2

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Sequence conservation between huGLC1A and moGLC1A

1	huGLC1A	MRFFCARCCS	FGPEMPAVQL	LLLACLWVDV	GARTAOQLRKA	NDQSGRCQYT
	moGLC1A		MPALHL	LFLACLWGM	GARTAOFRKA	NDRSGRCQYT
H						
51	huGLC1A	FSVASPNSS	CPEQSQAMSV	IHNLRDSST	QRDLLEATKA	RLSSLESLLH
	moGLC1A	FTVASPNSS	CPREDQAMSA	IQDLORDSSI	QHADLESTKA	RVRSLLESLLH
C						
101	huGLC1A	QLTLDOAARP	QETOEGLORE	LGTLRERDQ	LETQTRELET	AYSNLLRDKS
	moGLC1A	QMTLGRVTGT	QEAQEGLOGQ	LGALRRERDQ	LETQTRDLEA	AYNLLRDKS
151	huGLC1A	VLEEEKRRLR	QENENLARRL	ESSSQEVARL	RRGQCPQTRD	TARAVPPGSR
	moGLC1A	ALEEEKRQLE	QENEDLARRL	ESSSEEVTRL	RRGQCPSTQY	PSQDMLPGSR
201	huGLC1A	EVSTWMLDTL	AFQELKSELT	EVPASRIKKE	SPSGYLRSGE	GDTGCGELVW
	moGLC1A	EVSQWMLDTL	AFQELKSELT	EVPASQILKE	NPSGRPRSKKE	GDKGCGALVW
251	huGLC1A	VGEPLTLRTA	ETITGKYGVW	MRDPKPTYPY	TQETTWIRIDT	VGTDVROVFE
	moGLC1A	VGEPVTLRTA	ETIAGKYGVW	MRDPKPTHPY	TQESTWIRIDT	VGTEIROVFE
301	huGLC1A	YDLISQFMQG	YPSKVHILPR	PLESTGAVVY	SGSLYFOGAE	SRTVIRYELN
	moGLC1A	YSQISQFEQG	YPSKVHVLPR	ALESTGAVVY	AGSLYFOGAE	SRTVVRIELD
351	huGLC1A	TETVKAKEI	PGAGYHGQFP	YSWGGYTDID	LAVDEAGLWV	IYSTDEAKGA
	moGLC1A	TETVKAKEI	PGAGYHGHP	YANGGYTDID	LAVDESGLWV	IYSTEEAKGA
401	huGLC1A	IVLSKLNPEN	LELEQTWETN	IRKQSVANAF	IICGTLTYVS	SYTSADATVN
	moGLC1A	IVLSKLNPAN	LELERTWETN	IRKQSVANAF	VICGILTYVS	SYSSAHATVN
451	huGLC1A	FAYDTGTGIS	KTLTIPFKNR	YKYSSMIDYN	PLEKRLFAWD	NLNMVITYDIK
	moGLC1A	FAYDTKTGTS	KTLTIPFTNR	YKYSSMIDYN	PLERKLFWD	NFNMVITYDIK
501	huGLC1A	LSKM				
	moGLC1A	LLEM				

Fig. 3

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Sequence conservation between huGLC1A and moGLC1A

		H					
1	huGLC1A	MRFFCARCCS	FGPEMPAVOL	LLLACLVWDV	GARTAOQLRKA	NDQSGRCQYT	
			*** *	* *****	***** **	** *****	
	moGLC1A		MPALHL	LFLACLVWGM	GARTAOFRKA	NDRSGRCQYT	
		C					
51	huGLC1A	FSVASPNESS	CPEQSQAMSV	IHNLRQDSST	QRDLLEATKA	RLSSLESLLK	
		* *****	** ****	* *****	* *** **	* *****	
	moGLC1A	FTVASPNESS	CPREDQAMSA	IQDLQRDSSI	QHADLESTKA	RVRLESLELL	
101	huGLC1A	QLTLDQAARP	QETQEGLORE	LGTLRERERDQ	LETQTRELET	AYSNLLRDKS	
		* **	** *****	** *****	***** **	** *****	
	moGLC1A	QMTLGRVTGT	QEAQEGLOQO	LGALRRERDQ	LETQTRDLEA	AYNNLLRDKS	
151	huGLC1A	VLEEEKRLR	QENENLARRL	ESSSQEVARL	RRGQCPQTRD	TARAVPPGSR	
		***** *	**** *****	***** **	***** *	*****	
	moGLC1A	ALEEEKROLE	QENEDLARRL	ESSSEEVTRL	RRGQCPSTQY	PSQDMLPGSR	
201	huGLC1A	EVSTWNLDL	AFQELKSELT	EVPASRIKE	SPSGYLRSGE	GDTCGGELWV	
		*** *****	*****	*****	*** **	** *****	
	moGLC1A	EVSQWNLDL	AFQELKSELT	EVPASQILKE	NPSGRPRSKE	GDKGCGALWV	
		R K					
251	huGLC1A	VGEPLTLRTA	ETITGKYGVW	MRDPKPTYPY	TQETTWRIIDT	VGTDVROVFE	
		*** *****	*** *****	***** **	*** *****	*** *****	
	moGLC1A	VGEPTVTLRTA	ETIAGKYGVW	MRDPKPTHPY	TQESTWRIIDT	VGTEIROVFE	
301	huGLC1A	YDLISQFMQG	YPSKVHILPR	PLESTGAVVY	SGSLYFOGAE	SRTVIRYELN	
		* *** **	***** **	*****	*****	*** **	
	moGLC1A	YSQISQFEQG	YPSKVHVLPR	ALESTGAVVY	AGSLYFOGAE	SRTVVRYELD	
		S V 1 M G 2					
351	huGLC1A	TETVKAKEI	PGAGYHGQFP	YSWGGYTDID	LAVDEAGLWV	IYSTDEAKGA	
		*****	***** **	* *****	*****	*** *****	
	moGLC1A	TETVKAKEI	PGAGYHGHP	YANGGYTDID	LAVDESGLWV	IYSTEEAKGA	
		H H V					
401	huGLC1A	IVLSKLNPN	LELEQTWETN	IRKQSVANAF	IICGTLTYVS	SYTSADATVN	
		***** *	**** *****	*****	*** *****	** ** *	
	moGLC1A	IVLSKLNPN	LELERTWETN	IRKQSVANAF	VICGILTYVS	SYSSAHATVN	
		C N R					
451	huGLC1A	FAYDTGTGIS	KTLTIPFKNR	YKYSSMIDYN	PLEKKLFAWD	NLNMVITYDIK	
		***** **	***** **	*****	*** *****	*****	
	moGLC1A	FAYDTKTGTS	KTLTIPFTNR	YKYSSMIDYN	PLERKLFAWD	NFNMVITYDIK	
501	huGLC1A	LSKM					
		* *					
	moGLC1A	LLEM					

Fig. 3

SEQUENCE LISTING

5

(1) GENERAL INFORMATION:

- 10 (i) APPLICANT: Stone, Edwin M.
Sheffield, Val C.
Alward, Wallace L.M.
Fingert, John
- (ii) TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
- 15 (iii) NUMBER OF SEQUENCES: 43
- (iv) CORRESPONDENCE ADDRESS:
20 (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
(B) STREET: One Post Office Square
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109-2170
- 25 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US Unassigned
(B) FILING DATE: Concurrently Herewith
- 35 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Arnold, Beth E.
(B) REGISTRATION NUMBER: 35,430
(C) REFERENCE/DOCKET NUMBER: UIA-010.28
- 40 (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617-832-1000
(B) TELEFAX: 617-832-7000

45 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 2800 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	AGCGCAGGGG	AGGAGAAGAA	AAGAGAGGGA	TAGTGTATGA	GCAAGAAAGA	CAGATTCATT	60
5	CAAGGGCAGT	GGGAATTGAC	CACAGGGATT	ATAGTCCACG	TGATCCTGGG	TTCTAGGAGG	120
	CAGGGCTATA	TTGTGGGGGG	AAAAAATCAG	TTCAAGGGAA	GTCGGGAGAC	CTGATTTCTA	180
	ATACTATATT	TTTCCTTTAC	AAGCTGAGTA	ATTCTGAGCA	AGTCACAAGG	TAGTAACTGA	240
10	GGCTGTAAGA	TTACTTAGTT	TCTCCTTATT	AGGAACTCTT	TTTCTCTGTG	GAGTTAGCAG	300
	CACAAGGGCA	ATCCCGTTTC	TTTAAACAGG	AAGAAAACAT	TCCTAAGAGT	AAAGCCAAAC	360
15	AGATTCAAGC	CTAGGTCTTG	CTGACTATAT	GATTGGTTTT	TTGAAAAATC	ATTTTCAGCGA	420
	TGTTTACTAT	CTGATTCAGA	AAATGAGACT	AGTACCCTTT	GGTCAGCTGT	AAACAAACAC	480
	CCATTTGTAA	ATGTCTCAAG	TTCAGGCTTA	ACTGCAGAAC	CAATCAAATA	AGAATAGAAT	540
20	CTTTAGAGCA	AACTGTGTTT	CTCCACTCTG	GAGGTGAGTC	TGCCAGGGCA	GTTTGGAAAT	600
	ATTTACTTCA	CAAGTATTGA	CACGTGTGTT	GGTATTAACA	ACATAAAGTT	GCTCAAAGGC	660
25	AATCATTATT	TCAAGTGGCT	TAAAGTTACT	TCTGACAGTT	TTGGTATATT	TATTGGCTAT	720
	TGCCATTTGC	TTTTTGTTTT	TTCTCTTTGG	GTTTATTAAT	GTAAAGCAGG	GATTATTAAC	780
	CTACAGTCCA	GAAAGCCTGT	GAATTTGAAT	GAGGAAAAAA	TTACATTTTT	GTTTTTACCA	840
30	CCTTCTAACT	AAATTTAACA	TTTTATTCCA	TTGCGAATAG	AGCCATAAAC	TCAAAGTGGT	900
	AATAACAGTA	CCTGTGATTT	TGTCATTACC	AATAGAAATC	ACAGACATTT	TATACTATAT	960
35	TACAGTTGTT	GCAGATACGT	TGTAAGTGAA	ATATTTTATAC	TCAAAACTAC	TTTGAAATTA	1020
	GACCTCCTGC	TGGATCTTGT	TTTTAACATA	TTAATAAAAC	ATGTTTAAAA	TTTTGATATT	1080
	TTGATAATCA	TATTTTCATTA	TCATTTGTTT	CCTTTGTAAT	CTATATTTTA	TATATTTGAA	1140
40	AACATCTTTC	TGAGAAGAGT	TCCCCAGATT	TCACCAATGA	GGTTCTTGGC	ATGCACACAC	1200
	ACAGAGTAAG	AACTGATTTA	GAGGCTAACA	TTGACATTGG	TGCCTGAGAT	GCAAGACTGA	1260
45	AATTAGAAAG	TTCTCCCAAA	GATACACAGT	TGTTTTTAAAG	CTAGGGGTGA	GGGGGGAAAT	1320
	CTGCCGCTTC	TATAGGAATG	CTCTCCCTGG	AGCCTGGTAG	GGTGCTGTCC	TTGTGTTCTG	1380
	GCTGGCTGTT	ATTTTTCTCT	GTCCCTGCTA	CGTCTTAAAG	GACTTGTTTG	GATCTCCAGT	1440
50	TCCTAGCATA	GTGCCTGGCA	CAGTGCAGGT	TCTCAATGAG	TTTGCAGAGT	GAATGGAAAT	1500
	ATAAACTAGA	AATATATCCT	TGTTGAAATC	AGCACACCAG	TAGTCCTGGT	GTAAGTGTGT	1560
55	GTACGTGTGT	GTGTGTGTGT	GTGTGTGTGT	GTAAAACCAG	GTGGAGATAT	AGGAACTATT	1620

ATTGGGGTAT GGGTGCATAA ATTGGGATGT TCTTTTTTAAA AAGAAACTCC AAACAGACTT 1680
CTGGAAGGTT ATTTTCTAAG AATCTTGCTG GCAGCGTGAA GGCAACCCCC CTGTGCACAG 1740
5 CCCCACCCAG CCTCACGTGG CCACCTCTGT CTTCCCCCAT GAAGGGCTGG CTCCCCAGTA 1800
TATATAAACC TCTCTGGAGC TCGGGCATGA GCCAGCAAGG CCACCCATCC AGGCACCTCT 1860
CAGCACAGCA GAGCTTTCCA GAGGAAGCCT CACCAAGCCT CTGCAATGAG GTTCTTCTGT 1920
10 GCACGTTGCT GCAGCTTTGG GCCTGAGATG CCAGCTGTCC AGCTGCTGCT TCTGGCCTGC 1980
CTGGTGTGGG ATGTGGGGGC CAGGACAGCT CAGCTCAGGA AGGCCAATGA CCAGAGTGGC 2040
15 CGATGCCAGT ATACCTTCAG TGTGGCCAGT CCAATGAAT CCAGCTGCCC AGAGCAGAGC 2100
CAGGCCATGT CAGTCATCCA TAACTTACAG AGAGACAGCA GCACCCAACG CTTAGACCTG 2160
GAGGCCACCA AAGCTCGACT CAGCTCCCTG GAGAGCCTCC TCCACCAATT GACCTTGGAC 2220
20 CAGGCTGCCA GGCCCCAGGA GACCCAGGAG GGGCTGCAGA GGGAGCTGGG CACCCTGAGG 2280
CGGGAGCGGG ACCAGCTGGA AACCCAAACC AGAGAGTTGG AGACTGCCTA CAGCAACCTC 2340
25 CTCCGAGACA AGTCAGTTCT GGAGGAAGAG AAGAAGCGAC TAAGGCAAGA AAATGAGAAT 2400
CTGGCCAGGA GGTTGGAAAG CAGCAGCCAG GAGGTAGCAA GGCTGAGAAG GGGCCAGTGT 2460
CCCCAGACCC GAGACACTGC TCGGGCTGTG CCACCAGGCT CCAGAGAAGG TAAGAATGCA 2520
30 GAGTGGGGGG ACTCTGAGTT CAGCAGGTGA TATGGCTCGT AGTGACCTGC TACAGGCGCT 2580
CCAGGCCCTCC CTGCCTGCCC TTTCTCCTAG AGACTGCACA GCTAGCACAA GACAGATGAA 2640
35 TTAAGGAAAG CACAGCGATC ACCTTCAAGT ATTACTAGTA ATTTAGCTCC TGAGAGCTTC 2700
ATTTAGATTA GTGGTTCAGA GTTCTTGTGC CCCTCCATGT CAGTTTTTCAC AGTCCATAGC 2760
AAAAGGAGAA ATAAAAGGAC CGGGTGAGAT GTGTCTGCAT 2800

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 680 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: DNA (genomic)

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACCATGTTG GCCAGGCTGG TCTCGAACTC CTGACCTCAG GTGATCCGCC TGCCTCGGCC 60

TCCCAAAGTG CTGGGATTAC AGGCATGAGC CACCACGCCT GGCCGGCAGC CTATTTAAAT 120
GTCATCCTCA ACATAGTCAA TCCTTGGGCC ATTTTTTCTT ACAGTAAAAT TTTGTCTCTT 180
5 TCTTTTAATG CAGTTTCTAC GTGGAATTTG GACACTTTGG CCTTCCAGGA ACTGAAGTCC 240
GAGCTAACTG AAGTTCCTGC TTCCCGAATT TTGAAGGAGA GCCCATCTGG CTATCTCAGG 300
AGTGGAGAGG GAGACACCGG TATGAAGTTA AGTTTCTTCC CTTTTGTGCC CACATGGTCT 360
10 TTATTCATGT CTAGTGCTGT GTTCAGAGAA TCAGTATAGG GTAAATGCCC ACCCAAGGGG 420
GAAATTAAct TCCCTGGGAG CAGAGGGAGG GGAGGAGAAG AGGAACAGAA CTCTCTCTCT 480
CTCTCTGTTC CCTTGTGAGA GCAGGTCTGC AGGAGTCAGC CTTTCCCTAA CAAAGCCCTC 540
TATCCTATCA CCCACACTTG GGAGGCTGGG CTGGGCTGCA CAGGGCAAGA TGAGAGATGT 600
GTTGATTTCA TCCACTTGAT TGTCATGTAG AATTAGATAT ACTTGAGAAG TTACATTTTT 660
20 CAGTAGCGCC TTCATATCTT 680

(2) INFORMATION FOR SEQ ID NO:3:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2000 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTACAACTG ATACTGAGTG AATTGTACTT TAAATATTTT ATAGCTCCCA CTCCCATGCA 60
40 TGCCCCTCAG TGATAGCAAT AATTGTCAAT AACATGAAAC ACAGATTGAT CATATAGCAT 120
TTACCATATA TTTACTCTAT ACCAAGCACT TAACATATAT AATTACATTT AAAATTTACA 180
ACAGCCCTAC TACCCAAAAC ACTATTAGTA TCCCCTTTTA CACATGCGAT AACTGAGGCG 240
45 TAGAGAGCTA AGTAACTTAC TGAAAGTCAC ACAGCCAGCG GGTGGTAGAG CCTAGCTTTA 300
AACCCAGACG ATTTGTCTCC AGGGCTGTCA CATCTACTGG CTCTGCCAAG CTTCCGCATG 360
50 ATCATTGTCT GTGTTTGGAA AGATTATGGA TTAAGTGGTG CTTCGTTTTT TTTTCTGAAT 420
TTACCAGGAT GTGGAGAACT AGTTTGGGTA GGAGAGCCTC TCACGCTGAG AACAGCAGAA 480
ACAATTACTG GCAAGTATGG TGTGTGGATG CGAGACCCCA AGCCACCTA CCCCTACACC 540
55 CAGGAGACCA CGTGGAGAAT CGACACAGTT GGCACGGATG TCCGCCAGGT TTTTGAGTAT 600

GACCTCATCA GCCAGTTTAT GCAGGGCTAC CCTTCTAAGG TTCACATACT GCCTAGGCCA 660
CTGGAAAGCA CGGGTGCTGT GGTGTACTCG GGGAGCCTCT ATTTCCAGGG CGCTGAGTCC 720
5 AGAACTGTCA TAAGATATGA GCTGAATACC GAGACAGTGA AGGCTGAGAA GGAAATCCCT 780
GGAGCTGGCT ACCACGGACA GTTCCCGTAT TCTTGGGGTG GCTACACGGA CATTGACTTG 840
10 GCTGTGGATG AAGCAGGCCT CTGGGTCATT TACAGCACCG ATGAGGCCAA AGGTGCCATT 900
GTCTCTCCA AACTGAACCC AGAGAATCTG GAACTCGAAC AAACCTGGGA GACAAACATC 960
CGTAAGCAGT CAGTCGCCAA TGCCTTCATC ATCTGTGGCA CCTGTACAC CGTCAGCAGC 1020
15 TACACCTCAG CAGATGCTAC CGTCAACTTT GCTTATGACA CAGGCACAGG TATCAGCAAG 1080
ACCCTGACCA TCCCATTCAA GAACCGCTAT AAGTACAGCA GCATGATTGA CTACAACCCC 1140
CTGGAGAAGA AGCTCTTTGC CTGGGACAAC TTGAACATGG TCACTTATGA CATCAAGCTC 1200
20 TCCAAGATGT GAAAAGCCTC CAAGCTGTAC AGGCAATGGC AGAAGGAGAT GCTCAGGGCT 1260
CCTGGGGGGA GCAGGCTGAA GGGAGAGCCA GCCAGCCAGG GCCCAGGCAG CTTTGACTGC 1320
25 TTTCCAAGTT TTCATTAATC CAGAAGGATG AACATGGTCA CCATCTAACT ATTCAGGAAT 1380
TGTAAGTCTGA GGGCGTAGAC AATTTTCATAT AATAAATATC CTTTATCTTC TGTCAGCATT 1440
TATGGGATGT TTAATGACAT AGTTCAAGTT TTCTTGTGAT TTGGGGCAAA AGCTGTAAGG 1500
30 CATAATAGTT TCTTCCTGAA AACCATTGCT CTTGCATGTT ACATGGTTAC CACAAGCCAC 1560
AATAAAAAGC ATAACCTCTA AAGGAAGCAG AATAGCTCCT CTGGCCAGCA TCGAATATAA 1620
35 GTAAGATGCA TTTACTACAG TTGGCTTCTA ATGCTTCAGA TAGAATACAG TTGGGTCTCA 1680
CATAACCCTT TACATTGTGA AATAAAATTT TCTTACCCAA CGTTCTCTTC CTTGAACTTT 1740
GTGGGAATCT TTGCTTAAGA GAAGGATATA GATTCCAACC ATCAGGTAAT TCCTTCAGGT 1800
40 TGGGAGATGT GATTGCAGGA TGTAAAGGT GGTGTGTGTG TGTGTGTGTG TGTGTGTAAAC 1860
TGAGAGGCTT GTGCCTGGTT TTGAGGTGCT GCCCAGGATG ACGCCAAGCA AATAGCAGCA 1920
45 TCCACACTTT CCCACCTCCA TCTCCTGGTG CTCTCGGCAC TACCGGAGCA ATCTTTCCAT 1980
CTCTCCCCTG AACCCACCCT 2000

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2800 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	TACCTGGTAC	TTGTTGGCTG	GCCAATCTAA	CCAAATCAGT	GATCCCCAAG	CTCAGCGAGA	60
10	CAATCCGTCT	CAAAAAACA	AAGTGGAGAA	TGAAAGAAGA	CAACGCCTGA	CATAAGCCTC	120
	TAGCTCACAC	ACACACACAC	ACACACACGC	CTATACACAT	GAGTGTGCAC	CCACCCAGGT	180
	GAACGCAGAT	GCACACATAC	CCCACCCACA	CAAGAATGGA	TTTAGAGCAA	GAGGCACTTG	240
15	CTCAGTCTTC	AGGCGAATCT	GCTATGGGAA	CATCAGAGAA	ATTTATCACA	CAGATATCAC	300
	AAATGCTATT	ATTAGTATCT	GAGAACCAAG	TTGCTCAAAT	GCAAATGTTG	CTCTAAGGAA	360
20	CCCATGAGGG	GGCAGTGAGG	TGGCTGAGAG	GGGGAGGTGC	TTAGTGAGCA	GGCCTTACAG	420
	ACTGAGGTCA	GTCCCTAAAG	CCCATGCCAG	GAGGAGAGAA	CTGGACCCCA	AAAGTTGTCC	480
	TCTGACCACA	ACACGGCATG	CATGGCCCAT	GTGTGCTCAT	ATACCCCCCA	TATGAGCACA	540
25	CACCAGTAAG	TAAACATTTA	TAAAGATGTT	CATGAGGCTT	CCACGCACAC	ACTGGCTTAT	600
	GTGAACTTCT	GACAAGCCTT	GGTACTTGGT	ACTTGGTTCT	CCTGCTTGGT	TTTGGTTTTT	660
30	TTCATTTATC	TTATTTTTTT	ATTTGGAGGA	AGGTGTGTGT	GTGTGTGTGT	CTCTCTGTGT	720
	GTGTGTCTGT	GTGTGTGTGT	GTGTGTTGTT	GTTGTTGTTG	TTGTTGACAG	TTTCTTTTTT	780
	TAGGAGAAGT	CTCATTATAC	TGCCCAGTTG	TTCTTGAACT	CTTTTGTAGA	CTTAACAATT	840
35	CCCTTACATT	GCATTCAAAG	TAGTGGGCTC	TCTTTGAAAA	GGGAGTACTA	TTAGCTTACA	900
	GCCCGTGAAT	TTGAATTAGT	AAGTAAACTA	AATCTCCATT	TTCACAACCT	TCTCACTCAG	960
40	TTATTTTCATC	TCCTCATGGA	TAGCTACCTA	AACCTAAAGT	TATGATAACA	ATACCTGTAT	1020
	TTTCATCCCT	ATGTTACAGT	TGATACAGGT	TTCATGAAAT	ACTGTGTATA	CTCAAAAGTA	1080
	CTTTAAAATT	AAGCCTTATG	TTGAATAGCT	TATGTAGCAT	ACACTTCTGG	CATTTAAATA	1140
45	TTTTCATATT	GCTAACTAAA	TAACGTGTTT	CTTTGAGTCC	TTACGTTTTA	TACGTTTGGA	1200
	GTTATCTTTC	AGAGGTGGGC	ACACAGGTTT	CACCCGTAGG	GTTTGGGGGG	CACACTCATC	1260
50	CTAAAGCCTG	GTCCAGAGCA	TTGGCACAGG	TTCCTGAGAC	AAGAGCTGTG	GTTAGGGAGC	1320
	TTTTCTGAGG	ATGTTACACAG	GTTTATTCTA	AATCTAGGGC	AACATCATGT	TCTCATCCCC	1380
	TCTGTAGGAA	CCAGGAGCCT	GGAGGCATTG	GGCTCTCCTT	TGGACTCTTC	TTCGTCTCTG	1440
55	CTACAGGACG	TGTCTACTCA	GGCATGTCTG	TCTCCCTAGT	TCCTTATGCT	GGTCCAGTGA	1500

AACACAAAAT AGACTTATAT CCCTGTTCAA ACTAGCACAC AACCAGCTTC TCCTGTCAGA 1560
CAAGGTGCGC ATATGTTTAC AAGCACACAC AAACAGACTA GAAACTTAGG GGTATTATT 1620
5 GGGATGTGGG GTACATGCAC GGGGACTTCT AAAAAGAAAA TAAATTCAAA ATAGCCTCCG 1680
GCACTTTGTT TTAAAGACT CTTGCTGGCA GTGTGAGTGT AATCCTCCTA TCCCCCATG 1740
GCTGGTCCAA CCCAGCTTCA TGTGATCACC TCTCCCTCCC TCCACACAGG GCTGGGTCCC 1800
10 CAGGATATAT AAATGTCTTT GGACTTCAGG CTTGAGCCAG CAGGGCCACC CATCCAGACA 1860
CCTTGCAGGA GAACTTTCCA GAAGAAACCT CACCCAGCCT CCACACTGCT GTCCTTCTCT 1920
15 GCACGCTGCT GCAGCTGTGG TCCCAAGATG CCAGCTCTCC ATCTGCTGTT TCTGGCCTGC 1980
TTGGTGTGGG GAATGGGGG CAGGACAGCA CAGTTCGAA AGGCCAATGA TCGGAGTGGC 2040
CGATGCCAAT ACACCTTAC TGTGGCCAGC CCAATGAAT CTAGCTGCCC AAGGGAGGAC 2100
20 CAGGCCATGT CAGCCATCCA AGACCTTCAG AGAGACAGCA GCATCCAGCA TGCAGACCTA 2160
GAGTCCACCA AGGCCCGGGT CAGATCCCTG GAGAGTCTCC TCCACCAGAT GACCTTGGGC 2220
25 CGAGTTACTG GGACCCAGGA GGCCCAAGAG GGGCTGCAGG GCCAGTTGGG TGCCCTGAGG 2280
AGAGAACGGG ACCAGCTGGA GACCCAAACC AGGGATCTGG AGGCAGCCTA TAACAATCTC 2340
CTTCGAGATA AGTCGGCTTT AGAGGAAGAG AAGAGGCAGC TGAACAAGA GAATGAAGAT 2400
30 TTGGCCAGGA GGCTAGAAAG CAGCAGCGAG GAGGTAACAA GGCTGCGGAG GGGCCAGTGT 2460
CCTTCCACCC AGTACCCCTC TCAGGACATG CTGCCAGGCT CCAGGGAAGG TAAGAGTGCA 2520
35 GGGTGGAGTG GCCACCTGAC CCAGAAGGTA GCAAGTTTGC TGGTGACCCA TTACAGGACC 2580
CCCAGGCTTC TCCTTCTGTT TTGTCTTTTC TCTCAGAAAC TGCAAATCCA GCATGCAGTA 2640
GTTTCATTAA GGAGAGCAAA GCAAACACTT TTGCATGCTT CTAGAAAGTT GGCTCCTTGT 2700
40 TTAGGTCAGT GGATCTGAGC TCTTGTGCCC AGTCATGACA AAATGATCAT GGCCACAGC 2760
CAAATGACAA ACATGGGGCC AGGTGGCAGA TACATATGAT 2800

45 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	AAGCTTTT	TAATTATG	CCAAATTT	CTCCCC	ATTGAGAC	CAATCACC	CTAGTTCC	AGAGCTCA	60
5	TACCAACG	TGTTCAG	TTCATG	TTCATG	TCATGAG	CAACAGTA	TATTTG	GGGACAT	120
	CATCACC	CTCACAG	AGTCCG	TTCCTT	GTGTGTC	CTTTCT	ACTACT	ACAAGTG	180
	TCCTTT	GAAATC	AGTCTCT	CAAGTGT	GTGGAA	TTTGAC	ACGTTG	GCCTTC	240
10	GAGTTAA	CTGAGG	TTCTCC	CAATTC	TTGAAG	GAAATC	ATCCAT	CTGGCC	300
	AGCAAAG	AAGAGC	AAAGAT	TATGAA	GTGACT	TTCTCC	CTTTG	AGCCTT	360
15	CTCTCC	CTCTCT	CTCTCT	CTCTCT	CTCTCT	CTCTCT	CTCTCT	CTCTCT	420
	CCCTCT	CTCTCT	CTCTCT	CTCTCT	CTCTCT	CTCTCT	CTCTCT	CTCTCT	480
	ATGTGT	GTGTGT	GTGTGT	GTGTGT	GTGTGT	GTGTGT	GTGTGT	GTGTGT	540
20	TGTTCT	GTGTGT	GTGTGT	GTGTGT	GTGTGT	GTGTGT	GTGTGT	GTGTGT	600
	CCAAGG	CAGAGG	AGAGAG	CAAGAG	CAAGAG	CAAGAG	CAAGAG	CAAGAG	660
25	TACTGGA	AGCCTT	GGGAGC	CAACCT	TTGGA				680

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1456 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

	CTTTGTCT	ATCAAGG	AAAGAG	CTCATT	TGTGCT	CTCAAAAA	AAAAAAAA	AAAAGT	GTTC	60
	GATAGAA	ATATGG	CTGTGT	TTCCAG	AAAAAA	TAACATT	GACATG	TGTTTT	TATTA	120
45	CTAACAC	TGAGT	CTATGT	AGAGG	CTAACA	CGGAAG	GGGTAT	TGTTG	AGGGG	180
	CTCACAC	AGACAT	AGCAAT	GGCAAA	ACACCA	CAATGC	ACACAA	AAAAGA	AAAAAA	240
50	AGTCAAG	GCTCAC	AGAGAG	CTAGTA	AGTAC	CTCAC	ATGTG	GCATG	GTGAG	300
	AGAGGT	CAACCT	CTGTGC	TCTGCT	TTCTCT	CTGTTT	TTTGCC	ACTACT	GTCTC	360
	CTGTATT	CGGAAG	ACATAG	TACTAA	ATAAT	ATGGCA	ACTCT	CTCAG	T	420
55	TCATCAG	GATGTG	GAGCG	CTAGT	CTGGGT	GGAGAG	CCAGTC	ACCCTG	AGAGC	480

ACAATCGCTG GCAAGTATGG AGTGTGGATG AGAGACCCCA AGCCCACCCA CCCCTACACC 540
 CAGGAAAGCA CATGGAGGAT TGACACGGTT GGCACAGAGA TCCGCCAGGT GTTTGAGTAC 600
 5 AGTCAGATAA GCCAGTTCGA GCAGGGCTAT CTTTCCAAGG TCCATGTGCT CCCTCGGGCA 660
 CTGGAGAGCA CGGGTGCTGT GGTGTATGCG GGGAGCCTCT ATTTCCAGGG GGCTGAGTCC 720
 AGAACTGTGG TCAGGTATGA GCTAGACACG GAGACCGTGA AGGCAGAGAA GGAAATTCCT 780
 10 GGAGCTGGCT ACCACGGACA CTTCCCGTAC GCGTGGGGTG GCTACACAGA CATTGACTTA 840
 GCTGTGGATG AGAGCGGCCT CTGGGTCATC TACAGCACGG AGGAAGCCAA GGGGGCCATA 900
 15 GTCCTCTCCA AATTGAACCC AGCGAACCTG GAACTTGAGC GTACCTGGGA GACTAACATC 960
 CGTAAGCAGT CTGTGGCCAA TGCCTTTGTT ATCTGTGGCA TCTTGACAC GGTGAGCAGC 1020
 TACTCTTCAG CCCATGCAAC CGTCAACTTC GCCTACGACA CTAAAACGGG GACCAGTAAG 1080
 20 ACCCTGACCA TCCCATTCAC GAATCGCTAC AAGTACAGCA GTATGATTGA CTACAACCCC 1140
 CTGGAGAGGA AGCTGTTTGC CTGGGACAAC TTCAACATGG TCACCTATGA TATCAAGCTC 1200
 25 TTGGAGATGT GAGGAGCCTC TATGCCTACC AGCAAAGGCC AGAAAAGGTG AAGTTCCGGG 1260
 CTCCCGGGTG AAGCAGCTGT CAGCAGAGGC AGCCAGATGC ATGGAGTTTC TCCTCCTGCT 1320
 AAAGATTTTG TTTATCCGGG TCAATGTACA GCTAGCTCCC CTCTGACTGA CACGTCCTCC 1380
 30 AGGCTTGTAT AGTCGCATAG ACTCTGTTCT CTTCTGTCAG CTTTCAAAGG GCTGTTCCCTC 1440
 TTTTAAAAAT CACATA 1456

35 (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1515 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

45

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1512

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

55 ATG AGG TTC TTC TGT GCA CGT TGC TGC AGC TTT GGG CCT GAG ATG CCA 48
 Met Arg Phe Phe Cys Ala Arg Cys Cys Ser Phe Gly Pro Glu Met Pro
 1 5 10 15

	GCT	GTC	CAG	CTG	CTG	CTT	CTG	GCC	TGC	CTG	GTG	TGG	GAT	GTG	GGG	GCC	96
	Ala	Val	Gln	Leu	Leu	Leu	Leu	Ala	Cys	Leu	Val	Trp	Asp	Val	Gly	Ala	
				20					25					30			
5	AGG	ACA	GCT	CAG	CTC	AGG	AAG	GCC	AAT	GAC	CAG	AGT	GGC	CGA	TGC	CAG	144
	Arg	Thr	Ala	Gln	Leu	Arg	Lys	Ala	Asn	Asp	Gln	Ser	Gly	Arg	Cys	Gln	
			35					40					45				
10	TAT	ACC	TTC	AGT	GTG	GCC	AGT	CCC	AAT	GAA	TCC	AGC	TGC	CCA	GAG	CAG	192
	Tyr	Thr	Phe	Ser	Val	Ala	Ser	Pro	Asn	Glu	Ser	Ser	Cys	Pro	Glu	Gln	
			50				55					60					
15	AGC	CAG	GCC	ATG	TCA	GTC	ATC	CAT	AAC	TTA	CAG	AGA	GAC	AGC	AGC	ACC	240
	Ser	Gln	Ala	Met	Ser	Val	Ile	His	Asn	Leu	Gln	Arg	Asp	Ser	Ser	Thr	
	65					70					75					80	
20	CAA	CGC	TTA	GAC	CTG	GAG	GCC	ACC	AAA	GCT	CGA	CTC	AGC	TCC	CTG	GAG	288
	Gln	Arg	Leu	Asp	Leu	Glu	Ala	Thr	Lys	Ala	Arg	Leu	Ser	Ser	Leu	Glu	
					85					90					95		
	AGC	CTC	CTC	CAC	CAA	TTG	ACC	TTG	GAC	CAG	GCT	GCC	AGG	CCC	CAG	GAG	336
	Ser	Leu	Leu	His	Gln	Leu	Thr	Leu	Asp	Gln	Ala	Ala	Arg	Pro	Gln	Glu	
				100				105						110			
25	ACC	CAG	GAG	GGG	CTG	CAG	AGG	GAG	CTG	GGC	ACC	CTG	AGG	CGG	GAG	CGG	384
	Thr	Gln	Glu	Gly	Leu	Gln	Arg	Glu	Leu	Gly	Thr	Leu	Arg	Arg	Glu	Arg	
			115					120					125				
30	GAC	CAG	CTG	GAA	ACC	CAA	ACC	AGA	GAG	TTG	GAG	ACT	GCC	TAC	AGC	AAC	432
	Asp	Gln	Leu	Glu	Thr	Gln	Thr	Arg	Glu	Leu	Glu	Thr	Ala	Tyr	Ser	Asn	
		130					135					140					
35	CTC	CTC	CGA	GAC	AAG	TCA	GTT	CTG	GAG	GAA	GAG	AAG	AAG	CGA	CTA	AGG	480
	Leu	Leu	Arg	Asp	Lys	Ser	Val	Leu	Glu	Glu	Glu	Lys	Lys	Arg	Leu	Arg	
	145					150					155					160	
40	CAA	GAA	AAT	GAG	AAT	CTG	GCC	AGG	AGG	TTG	GAA	AGC	AGC	AGC	CAG	GAG	528
	Gln	Glu	Asn	Glu	Asn	Leu	Ala	Arg	Arg	Leu	Glu	Ser	Ser	Ser	Gln	Glu	
					165					170					175		
	GTA	GCA	AGG	CTG	AGA	AGG	GGC	CAG	TGT	CCC	CAG	ACC	CGA	GAC	ACT	GCT	576
	Val	Ala	Arg	Leu	Arg	Arg	Gly	Gln	Cys	Pro	Gln	Thr	Arg	Asp	Thr	Ala	
				180					185					190			
45	CGG	GCT	GTG	CCA	CCA	GGC	TCC	AGA	GAA	GTT	TCT	ACG	TGG	AAT	TTG	GAC	624
	Arg	Ala	Val	Pro	Pro	Gly	Ser	Arg	Glu	Val	Ser	Thr	Trp	Asn	Leu	Asp	
			195					200					205				
50	ACT	TTG	GCC	TTC	CAG	GAA	CTG	AAG	TCC	GAG	CTA	ACT	GAA	GTT	CCT	GCT	672
	Thr	Leu	Ala	Phe	Gln	Glu	Leu	Lys	Ser	Glu	Leu	Thr	Glu	Val	Pro	Ala	
			210				215					220					
55	TCC	CGA	ATT	TTG	AAG	GAG	AGC	CCA	TCT	GGC	TAT	CTC	AGG	AGT	GGA	GAG	720
	Ser	Arg	Ile	Leu	Lys	Glu	Ser	Pro	Ser	Gly	Tyr	Leu	Arg	Ser	Gly	Glu	
	225					230					235					240	

	GGA GAC ACC GGA TGT GGA GAA CTA GTT TGG GTA GGA GAG CCT CTC ACG	768
	Gly Asp Thr Gly Cys Gly Glu Leu Val Trp Val Gly Glu Pro Leu Thr	
	245 250 255	
5	CTG AGA ACA GCA GAA ACA ATT ACT GGC AAG TAT GGT GTG TGG ATG CGA	816
	Leu Arg Thr Ala Glu Thr Ile Thr Gly Lys Tyr Gly Val Trp Met Arg	
	260 265 270	
10	GAC CCC AAG CCC ACC TAC CCC TAC ACC CAG GAG ACC ACG TGG AGA ATC	864
	Asp Pro Lys Pro Thr Tyr Pro Tyr Thr Gln Glu Thr Thr Trp Arg Ile	
	275 280 285	
15	GAC ACA GTT GGC ACG GAT GTC CGC CAG GTT TTT GAG TAT GAC CTC ATC	912
	Asp Thr Val Gly Thr Asp Val Arg Gln Val Phe Glu Tyr Asp Leu Ile	
	290 295 300	
20	AGC CAG TTT ATG CAG GGC TAC CCT TCT AAG GTT CAC ATA CTG CCT AGG	960
	Ser Gln Phe Met Gln Gly Tyr Pro Ser Lys Val His Ile Leu Pro Arg	
	305 310 315 320	
25	CCA CTG GAA AGC ACG GGT GCT GTG GTG TAC TCG GGG AGC CTC TAT TTC	1008
	Pro Leu Glu Ser Thr Gly Ala Val Val Tyr Ser Gly Ser Leu Tyr Phe	
	325 330 335	
30	CAG GGC GCT GAG TCC AGA ACT GTC ATA AGA TAT GAG CTG AAT ACC GAG	1056
	Gln Gly Ala Glu Ser Arg Thr Val Ile Arg Tyr Glu Leu Asn Thr Glu	
	340 345 350	
35	ACA GTG AAG GCT GAG AAG GAA ATC CCT GGA GCT GGC TAC CAC GGA CAG	1104
	Thr Val Lys Ala Glu Lys Glu Ile Pro Gly Ala Gly Tyr His Gly Gln	
	355 360 365	
40	TTC CCG TAT TCT TGG GGT GGC TAC ACG GAC ATT GAC TTG GCT GTG GAT	1152
	Phe Pro Tyr Ser Trp Gly Gly Tyr Thr Asp Ile Asp Leu Ala Val Asp	
	370 375 380	
45	GAA GCA GGC CTC TGG GTC ATT TAC AGC ACC GAT GAG GCC AAA GGT GCC	1200
	Glu Ala Gly Leu Trp Val Ile Tyr Ser Thr Asp Glu Ala Lys Gly Ala	
	385 390 395 400	
50	ATT GTC CTC TCC AAA CTG AAC CCA GAG AAT CTG GAA CTC GAA CAA ACC	1248
	Ile Val Leu Ser Lys Leu Asn Pro Glu Asn Leu Glu Leu Glu Gln Thr	
	405 410 415	
55	TGG GAG ACA AAC ATC CGT AAG CAG TCA GTC GCC AAT GCC TTC ATC ATC	1296
	Trp Glu Thr Asn Ile Arg Lys Gln Ser Val Ala Asn Ala Phe Ile Ile	
	420 425 430	
60	TGT GGC ACC TTG TAC ACC GTC AGC AGC TAC ACC TCA GCA GAT GCT ACC	1344
	Cys Gly Thr Leu Tyr Thr Val Ser Ser Tyr Thr Ser Ala Asp Ala Thr	
	435 440 445	
65	GTC AAC TTT GCT TAT GAC ACA GGC ACA GGT ATC AGC AAG ACC CTG ACC	1392
	Val Asn Phe Ala Tyr Asp Thr Gly Thr Gly Ile Ser Lys Thr Leu Thr	
	450 455 460	

ATC CCA TTC AAG AAC CGC TAT AAG TAC AGC AGC ATG ATT GAC TAC AAC 1440
 Ile Pro Phe Lys Asn Arg Tyr Lys Tyr Ser Ser Met Ile Asp Tyr Asn
 465 470 475 480

5 CCC CTG GAG AAG AAG CTC TTT GCC TGG GAC AAC TTG AAC ATG GTC ACT 1488
 Pro Leu Glu Lys Lys Leu Phe Ala Trp Asp Asn Leu Asn Met Val Thr
 485 490 495

10 TAT GAC ATC AAG CTC TCC AAG ATG TGA
 1515
 Tyr Asp Ile Lys Leu Ser Lys Met
 500

15 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 504 amino acids
 (B) TYPE: amino acid
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

25 Met Arg Phe Phe Cys Ala Arg Cys Cys Ser Phe Gly Pro Glu Met Pro
 1 5 10 15

30 Ala Val Gln Leu Leu Leu Ala Cys Leu Val Trp Asp Val Gly Ala
 20 25 30

Arg Thr Ala Gln Leu Arg Lys Ala Asn Asp Gln Ser Gly Arg Cys Gln
 35 35 40 45

Tyr Thr Phe Ser Val Ala Ser Pro Asn Glu Ser Ser Cys Pro Glu Gln
 50 55 60

Ser Gln Ala Met Ser Val Ile His Asn Leu Gln Arg Asp Ser Ser Thr
 40 65 70 75 80

Gln Arg Leu Asp Leu Glu Ala Thr Lys Ala Arg Leu Ser Ser Leu Glu
 85 90 95

Ser Leu Leu His Gln Leu Thr Leu Asp Gln Ala Ala Arg Pro Gln Glu
 45 100 105 110

Thr Gln Glu Gly Leu Gln Arg Glu Leu Gly Thr Leu Arg Arg Glu Arg
 115 120 125

50 Asp Gln Leu Glu Thr Gln Thr Arg Glu Leu Glu Thr Ala Tyr Ser Asn
 130 135 140

55 Leu Leu Arg Asp Lys Ser Val Leu Glu Glu Glu Lys Lys Arg Leu Arg
 145 150 155 160

Gln Glu Asn Glu Asn Leu Ala Arg Arg Leu Glu Ser Ser Ser Gln Glu
 165 170 175
 5 Val Ala Arg Leu Arg Arg Gly Gln Cys Pro Gln Thr Arg Asp Thr Ala
 180 185 190
 Arg Ala Val Pro Pro Gly Ser Arg Glu Val Ser Thr Trp Asn Leu Asp
 195 200 205
 10 Thr Leu Ala Phe Gln Glu Leu Lys Ser Glu Leu Thr Glu Val Pro Ala
 210 215 220
 Ser Arg Ile Leu Lys Glu Ser Pro Ser Gly Tyr Leu Arg Ser Gly Glu
 225 230 235 240
 15 Gly Asp Thr Gly Cys Gly Glu Leu Val Trp Val Gly Glu Pro Leu Thr
 245 250 255
 20 Leu Arg Thr Ala Glu Thr Ile Thr Gly Lys Tyr Gly Val Trp Met Arg
 260 265 270
 Asp Pro Lys Pro Thr Tyr Pro Tyr Thr Gln Glu Thr Thr Trp Arg Ile
 275 280 285
 25 Asp Thr Val Gly Thr Asp Val Arg Gln Val Phe Glu Tyr Asp Leu Ile
 290 295 300
 Ser Gln Phe Met Gln Gly Tyr Pro Ser Lys Val His Ile Leu Pro Arg
 305 310 315 320
 30 Pro Leu Glu Ser Thr Gly Ala Val Val Tyr Ser Gly Ser Leu Tyr Phe
 325 330 335
 Gln Gly Ala Glu Ser Arg Thr Val Ile Arg Tyr Glu Leu Asn Thr Glu
 340 345 350
 35 Thr Val Lys Ala Glu Lys Glu Ile Pro Gly Ala Gly Tyr His Gly Gln
 355 360 365
 40 Phe Pro Tyr Ser Trp Gly Gly Tyr Thr Asp Ile Asp Leu Ala Val Asp
 370 375 380
 Glu Ala Gly Leu Trp Val Ile Tyr Ser Thr Asp Glu Ala Lys Gly Ala
 385 390 395 400
 45 Ile Val Leu Ser Lys Leu Asn Pro Glu Asn Leu Glu Leu Glu Gln Thr
 405 410 415
 50 Trp Glu Thr Asn Ile Arg Lys Gln Ser Val Ala Asn Ala Phe Ile Ile
 420 425 430
 Cys Gly Thr Leu Tyr Thr Val Ser Ser Tyr Thr Ser Ala Asp Ala Thr
 435 440 445
 55 Val Asn Phe Ala Tyr Asp Thr Gly Thr Gly Ile Ser Lys Thr Leu Thr

450 455 460
 Ile Pro Phe Lys Asn Arg Tyr Lys Tyr Ser Ser Met Ile Asp Tyr Asn
 465 470 475 480
 5 Pro Leu Glu Lys Lys Leu Phe Ala Trp Asp Asn Leu Asn Met Val Thr
 485 490 495
 10 Tyr Asp Ile Lys Leu Ser Lys Met
 500

(2) INFORMATION FOR SEQ ID NO:9:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1473 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 25 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

30 ATG CCA GCT CTC CAT CTG CTG TTT CTG GCC TGC TTG GTG TGG GGA ATG 48
 Met Pro Ala Leu His Leu Leu Phe Leu Ala Cys Leu Val Trp Gly Met
 1 5 10 15
 35 GGG GCC AGG ACA GCA CAG TTC CGA AAG GCC AAT GAT CGG AGT GGC CGA 96
 Gly Ala Arg Thr Ala Gln Phe Arg Lys Ala Asn Asp Arg Ser Gly Arg
 20 25 30
 40 TGC CAA TAC ACC TTC ACT GTG GCC AGC CCC AAT GAA TCT AGC TGC CCA 144
 Cys Gln Tyr Thr Phe Thr Val Ala Ser Pro Asn Glu Ser Ser Cys Pro
 35 40 45
 45 AGG GAG GAC CAG GCC ATG TCA GCC ATC CAA GAC CTT CAG AGA GAC AGC 192
 Arg Glu Asp Gln Ala Met Ser Ala Ile Gln Asp Leu Gln Arg Asp Ser
 50 55 60
 50 AGC ATC CAG CAT GCA GAC CTA GAG TCC ACC AAG GCC CGG GTC AGA TCC 240
 Ser Ile Gln His Ala Asp Leu Glu Ser Thr Lys Ala Arg Val Arg Ser
 65 70 75 80
 55 CTG GAG AGT CTC CTC CAC CAG ATG ACC TTG GGC CGA GTT ACT GGG ACC 288
 Leu Glu Ser Leu Leu His Gln Met Thr Leu Gly Arg Val Thr Gly Thr
 85 90 95
 55 CAG GAG GCC CAA GAG GGG CTG CAG GGC CAG TTG GGT GCC CTG AGG AGA 336
 Gln Glu Ala Gln Glu Gly Leu Gln Gly Gln Leu Gly Ala Leu Arg Arg
 100 105 110

	GAA CGG GAC CAG CTG GAG ACC CAA ACC AGG GAT CTG GAG GCA GCC TAT	384
	Glu Arg Asp Gln Leu Glu Thr Gln Thr Arg Asp Leu Glu Ala Ala Tyr	
	115 120 125	
5	AAC AAT CTC CTT CGA GAT AAG TCG GCT TTA GAG GAA GAG AAG AGG CAG	432
	Asn Asn Leu Leu Arg Asp Lys Ser Ala Leu Glu Glu Glu Lys Arg Gln	
	130 135 140	
10	CTG GAA CAA GAG AAT GAA GAT TTG GCC AGG AGG CTA GAA AGC AGC AGC	480
	Leu Glu Gln Glu Asn Glu Asp Leu Ala Arg Arg Leu Glu Ser Ser Ser	
	145 150 155 160	
15	GAG GAG GTA ACA AGG CTG CGG AGG GGC CAG TGT CCT TCC ACC CAG TAC	528
	Glu Glu Val Thr Leu Arg Arg Gly Gln Cys Pro Ser Thr Gln Tyr	
	165 170 175	
20	CCC TCT CAG GAC ATG CTG CCA GGC TCC AGG GAA GTC TCT CAG TGG AAT	576
	Pro Ser Gln Asp Met Leu Pro Gly Ser Arg Glu Val Ser Gln Trp Asn	
	180 185 190	
25	TTG GAC ACG TTG GCC TTC CAG GAA TTG AAG TCA GAG TTA ACT GAG GTT	624
	Leu Asp Thr Leu Ala Phe Gln Glu Leu Lys Ser Glu Leu Thr Glu Val	
	195 200 205	
30	CCT GCT TCC CAA ATC TTG AAG GAA AAT CCA TCT GGC CGA CCC AGG AGC	672
	Pro Ala Ser Gln Ile Leu Lys Glu Asn Pro Ser Gly Arg Pro Arg Ser	
	210 215 220	
35	AAA GAA GGA GAC AAA GGA TGT GGA GCG CTA GTC TGG GTA GGA GAG CCA	720
	Lys Glu Gly Asp Lys Gly Cys Gly Ala Leu Val Trp Val Gly Glu Pro	
	225 230 235 240	
40	GTC ACC CTG AGG ACA GCT GAA ACA ATC GCT GGC AAG TAT GGA GTG TGG	768
	Val Thr Leu Arg Thr Ala Glu Thr Ile Ala Gly Lys Tyr Gly Val Trp	
	245 250 255	
45	ATG AGA GAC CCC AAG CCC ACC CAC CCC TAC ACC CAG GAA AGC ACA TGG	816
	Met Arg Asp Pro Lys Pro Thr His Pro Tyr Thr Gln Glu Ser Thr Trp	
	260 265 270	
50	AGG ATT GAC ACG GTT GGC ACA GAG ATC CGC CAG GTG TTT GAG TAC AGT	864
	Arg Ile Asp Thr Val Gly Thr Glu Ile Arg Gln Val Phe Glu Tyr Ser	
	275 280 285	
55	CAG ATA AGC CAG TTC GAG CAG GGC TAT CCT TCC AAG GTC CAT GTG CTC	912
	Gln Ile Ser Gln Phe Glu Gln Gly Tyr Pro Ser Lys Val His Val Leu	
	290 295 300	
60	CCT CGG GCA CTG GAG AGC ACG GGT GCT GTG GTG TAT GCG GGG AGC CTC	960
	Pro Arg Ala Leu Glu Ser Thr Gly Ala Val Val Tyr Ala Gly Ser Leu	
	305 310 315 320	
65	TAT TTC CAG GGG GCT GAG TCC AGA ACT GTG GTC AGG TAT GAG CTA GAC	1008
	Tyr Phe Gln Gly Ala Glu Ser Arg Thr Val Val Arg Tyr Glu Leu Asp	
	325 330 335	

	ACG	GAG	ACC	GTG	AAG	GCA	GAG	AAG	GAA	ATT	CCT	GGA	GCT	GGC	TAC	CAC	1056
	Thr	Glu	Thr	Val	Lys	Ala	Glu	Lys	Glu	Ile	Pro	Gly	Ala	Gly	Tyr	His	
				340					345					350			
5	GGA	CAC	TTC	CCG	TAC	GCG	TGG	GGT	GGC	TAC	ACA	GAC	ATT	GAC	TTA	GCT	1104
	Gly	His	Phe	Pro	Tyr	Ala	Trp	Gly	Gly	Tyr	Thr	Asp	Ile	Asp	Leu	Ala	
			355					360					365				
10	GTG	GAT	GAG	AGC	GGC	CTC	TGG	GTC	ATC	TAC	AGC	ACG	GAG	GAA	GCC	AAG	1152
	Val	Asp	Glu	Ser	Gly	Leu	Trp	Val	Ile	Tyr	Ser	Thr	Glu	Glu	Ala	Lys	
		370					375					380					
15	GGG	GCC	ATA	GTC	CTC	TCC	AAA	TTG	AAC	CCA	GCG	AAC	CTG	GAA	CTT	GAG	1200
	Gly	Ala	Ile	Val	Leu	Ser	Lys	Leu	Asn	Pro	Ala	Asn	Leu	Glu	Leu	Glu	
	385					390					395					400	
20	CGT	ACC	TGG	GAG	ACT	AAC	ATC	CGT	AAG	CAG	TCT	GTG	GCC	AAT	GCC	TTT	1248
	Arg	Thr	Trp	Glu	Thr	Asn	Ile	Arg	Lys	Gln	Ser	Val	Ala	Asn	Ala	Phe	
				405						410					415		
	GTT	ATC	TGT	GGC	ATC	TTG	TAC	ACG	GTG	AGC	AGC	TAC	TCT	TCA	GCC	CAT	1296
	Val	Ile	Cys	Gly	Ile	Leu	Tyr	Thr	Val	Ser	Ser	Tyr	Ser	Ser	Ala	His	
				420					425					430			
25	GCA	ACC	GTC	AAC	TTC	GCC	TAC	GAC	ACT	AAA	ACG	GGG	ACC	AGT	AAG	ACC	1344
	Ala	Thr	Val	Asn	Phe	Ala	Tyr	Asp	Thr	Lys	Thr	Gly	Thr	Ser	Lys	Thr	
			435					440					445				
30	CTG	ACC	ATC	CCA	TTC	ACG	AAT	CGC	TAC	AAG	TAC	AGC	AGT	ATG	ATT	GAC	1392
	Leu	Thr	Ile	Pro	Phe	Thr	Asn	Arg	Tyr	Lys	Tyr	Ser	Ser	Met	Ile	Asp	
		450					455					460					
35	TAC	AAC	CCC	CTG	GAG	AGG	AAG	CTG	TTT	GCC	TGG	GAC	AAC	TTC	AAC	ATG	1440
	Tyr	Asn	Pro	Leu	Glu	Arg	Lys	Leu	Phe	Ala	Trp	Asp	Asn	Phe	Asn	Met	
	465					470					475					480	
40	GTC	ACC	TAT	GAT	ATC	AAG	CTC	TTG	GAG	ATG	TGA						1473
	Val	Thr	Tyr	Asp	Ile	Lys	Leu	Leu	Glu	Met							
					485					490							

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 490 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Pro Ala Leu His Leu Leu Phe Leu Ala Cys Leu Val Trp Gly Met
 1 5 10 15
 Gly Ala Arg Thr Ala Gln Phe Arg Lys Ala Asn Asp Arg Ser Gly Arg

	20					25					30					
	Cys	Gln	Tyr	Thr	Phe	Thr	Val	Ala	Ser	Pro	Asn	Glu	Ser	Ser	Cys	Pro
			35					40					45			
5	Arg	Glu	Asp	Gln	Ala	Met	Ser	Ala	Ile	Gln	Asp	Leu	Gln	Arg	Asp	Ser
		50					55					60				
10	Ser	Ile	Gln	His	Ala	Asp	Leu	Glu	Ser	Thr	Lys	Ala	Arg	Val	Arg	Ser
		65					70					75				80
	Leu	Glu	Ser	Leu	Leu	His	Gln	Met	Thr	Leu	Gly	Arg	Val	Thr	Gly	Thr
					85					90					95	
15	Gln	Glu	Ala	Gln	Glu	Gly	Leu	Gln	Gly	Gln	Leu	Gly	Ala	Leu	Arg	Arg
				100					105					110		
	Glu	Arg	Asp	Gln	Leu	Glu	Thr	Gln	Thr	Arg	Asp	Leu	Glu	Ala	Ala	Tyr
20			115					120					125			
	Asn	Asn	Leu	Leu	Arg	Asp	Lys	Ser	Ala	Leu	Glu	Glu	Glu	Lys	Arg	Gln
		130					135					140				
25	Leu	Glu	Gln	Glu	Asn	Glu	Asp	Leu	Ala	Arg	Arg	Leu	Glu	Ser	Ser	Ser
	145				150					155						160
	Glu	Glu	Val	Thr	Arg	Leu	Arg	Arg	Gly	Gln	Cys	Pro	Ser	Thr	Gln	Tyr
				165					170						175	
30	Pro	Ser	Gln	Asp	Met	Leu	Pro	Gly	Ser	Arg	Glu	Val	Ser	Gln	Trp	Asn
			180					185						190		
	Leu	Asp	Thr	Leu	Ala	Phe	Gln	Glu	Leu	Lys	Ser	Glu	Leu	Thr	Glu	Val
35		195					200					205				
	Pro	Ala	Ser	Gln	Ile	Leu	Lys	Glu	Asn	Pro	Ser	Gly	Arg	Pro	Arg	Ser
		210					215					220				
40	Lys	Glu	Gly	Asp	Lys	Gly	Cys	Gly	Ala	Leu	Val	Trp	Val	Gly	Glu	Pro
	225				230						235					240
	Val	Thr	Leu	Arg	Thr	Ala	Glu	Thr	Ile	Ala	Gly	Lys	Tyr	Gly	Val	Trp
				245					250						255	
45	Met	Arg	Asp	Pro	Lys	Pro	Thr	His	Pro	Tyr	Thr	Gln	Glu	Ser	Thr	Trp
			260					265						270		
	Arg	Ile	Asp	Thr	Val	Gly	Thr	Glu	Ile	Arg	Gln	Val	Phe	Glu	Tyr	Ser
50		275					280						285			
	Gln	Ile	Ser	Gln	Phe	Glu	Gln	Gly	Tyr	Pro	Ser	Lys	Val	His	Val	Leu
		290					295					300				
55	Pro	Arg	Ala	Leu	Glu	Ser	Thr	Gly	Ala	Val	Val	Tyr	Ala	Gly	Ser	Leu
	305				310					315						320

	Tyr	Phe	Gln	Gly	Ala	Glu	Ser	Arg	Thr	Val	Val	Arg	Tyr	Glu	Leu	Asp	
					325											335	
5	Thr	Glu	Thr	Val	Lys	Ala	Glu	Lys	Glu	Ile	Pro	Gly	Ala	Gly	Tyr	His	
				340					345					350			
	Gly	His	Phe	Pro	Tyr	Ala	Trp	Gly	Gly	Tyr	Thr	Asp	Ile	Asp	Leu	Ala	
			355					360					365				
10	Val	Asp	Glu	Ser	Gly	Leu	Trp	Val	Ile	Tyr	Ser	Thr	Glu	Glu	Ala	Lys	
		370					375						380				
	Gly	Ala	Ile	Val	Leu	Ser	Lys	Leu	Asn	Pro	Ala	Asn	Leu	Glu	Leu	Glu	
	385					390					395					400	
15	Arg	Thr	Trp	Glu	Thr	Asn	Ile	Arg	Lys	Gln	Ser	Val	Ala	Asn	Ala	Phe	
					405					410					415		
	Val	Ile	Cys	Gly	Ile	Leu	Tyr	Thr	Val	Ser	Ser	Tyr	Ser	Ser	Ala	His	
20				420					425					430			
	Ala	Thr	Val	Asn	Phe	Ala	Tyr	Asp	Thr	Lys	Thr	Gly	Thr	Ser	Lys	Thr	
			435					440					445				
25	Leu	Thr	Ile	Pro	Phe	Thr	Asn	Arg	Tyr	Lys	Tyr	Ser	Ser	Met	Ile	Asp	
		450					455					460					
	Tyr	Asn	Pro	Leu	Glu	Arg	Lys	Leu	Phe	Ala	Trp	Asp	Asn	Phe	Asn	Met	
	465					470					475					480	
30	Val	Thr	Tyr	Asp	Ile	Lys	Leu	Leu	Glu	Met							
					485					490							

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGGGCTGCA GAGGGAGCTG GGCACCCTG

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

10

ATACTGCCTA GGCCACTGGA

20

(2) INFORMATION FOR SEQ ID NO:13:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAATGTCCGT GTAGCCACC

19

30

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAACTCGAAC AAACCTGGGA

20

50

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

55

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CATGCTGCTG TACTTATAGC GG

22

10

- (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

20

25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCTGGCTCC CAGTATATA

20

30

- (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

40

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

45

ACAGCTGGCA TCTCAGGC

18

- (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

55

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACGTTGCTCC AGCTTTGG

18

(2) INFORMATION FOR SEQ ID NO:19:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGACTGAC ATGGCCTGG

19

25

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
35 (A) DESCRIPTION: /desc = "primer"

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGTGCCGAT GCCAGTATAC

20

(2) INFORMATION FOR SEQ ID NO:21:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTGGTCCAAG GTCAATTGGT

20

5 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15 (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

20

AGGCCATGTC AGTCATCCAT

20

(2) INFORMATION FOR SEQ ID NO:23:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCTCTGGTTT GGGTTTCCAG

20

40

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

45 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

50 (A) DESCRIPTION: /desc = "primer"

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGACCTTGGA CCAGGCTG

18

(2) INFORMATION FOR SEQ ID NO:25:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
10 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCTGGCCAGA TTCTCATTTT

20

20

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
30 (A) DESCRIPTION: /desc = "primer"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGAGGAAGA GAAGAAGCGA

20

40

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
45 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

55 CTGCTGAACT CAGAGTCCCC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AACATAGTCA ATCCTTGGGC C

21

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TAAAGACCAT GTGGGCACAA

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTATGGATTA AGTGGTGCTT CG

22

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

15 ATTCTCCACG TGGTCTCCTG

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AAGCCACCT ACCCCTACAC

20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

50

AATAGAGGCT CCCCAGGTAC A

21

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

55

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 5 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ATACTGCCTA GGCCACTGGA

20

- 15 (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 25 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"

- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CAATGTCCGT GTAGCCACC

19

- (2) INFORMATION FOR SEQ ID NO:36:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
40 (D) TOPOLOGY: linear

- 45 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TGGCTACCAC GGACACTTC

19

- 55 (2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

10

CATTGGCGAC TGACTGCTTA

20

(2) INFORMATION FOR SEQ ID NO:38:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAACTCGAAC AAACCTGGGA

20

30

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

45

CATGCTGCTG TACTTATAGC GG

22

(2) INFORMATION FOR SEQ ID NO:40:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGCAAGACCC TGACCATCC

19

10

- (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AGCATCTCCT TCTGCCATTG

20

25

- (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

35

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

40

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TTCCTTCAGG TTGGGAGATG

20

45

- (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

5

GAGAGCACCA GGAGATGGAG

20

INTERNATIONAL SEARCH REPORT

Intern: al Application No
PCT/US 99/07671

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	STONE E.M. ET AL.: "Identification of a gene that causes primary open angle glaucoma" SCIENCE, vol. 275, 1997, pages 668-670, XP002049424 US the whole document	1-13
X	KUBOTA R. ET AL.: "Genomic organisation of the human myocilin gene (MYOC) responsible for primary open angle glaucoma" BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 242, 1998, pages 396-400, XP002120488 us the whole document	1-13

☒ Further documents are listed in the continuation of box C.

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Date of the actual completion of the international search

28 October 1999

Date of mailing of the international search report

16/11/1999

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INTERNATIONAL SEARCH REPORT

Internat Application No

PCT/US 99/07671

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	KUBOTA R. ET AL.: "A novel myosin-like protein (myocilin) expressed in the connecting cilium of the photoreceptor: molecular cloning, tissue expression, and chromosomal mapping" GENOMICS, vol. 41, no. 3, 1 May 1997 (1997-05-01), pages 360-369, XP002120489 US the whole document	1-8
X	WO 96 14411 A (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA) 17 May 1996 (1996-05-17) page 36 -page 41; claims; figures	1
P,X	W.L.M. ALWARD ET AL.: "Clinical features associated with mutations in the chromosome 1 open-angle glaucoma gene (GLC1A)" THE NEW ENGLAND JOURNAL OF MEDICINE, vol. 338, 9 April 1998 (1998-04-09), pages 1022-1027, XP002120490 US the whole document	1-13
P,X	WO 98 32850 A (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA) 30 July 1998 (1998-07-30) the whole document	1-8
P,X	WO 98 20131 A (UNIVERSITY OF IOWA) 14 May 1998 (1998-05-14) the whole document esp. table 3	1-13

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 99/07671

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9614411 A	17-05-1996	US 5606043 A	25-02-1997
		AU 2432897 A	22-10-1998
		AU 705420 B	20-05-1999
		AU 4279296 A	31-05-1996
		CA 2204375 A	17-05-1996
		EP 0789762 A	20-08-1997
		JP 10509866 T	29-09-1998
		NO 972024 A	02-07-1997
		NZ 297601 A	29-04-1999
		WO 9844107 A	08-10-1998
		US 5849879 A	15-12-1998
		US 5789169 A	04-08-1998
		US 5861497 A	19-01-1999
		US 5854415 A	29-12-1998
		ZA 9509256 A	14-08-1996
WO 9832850 A	30-07-1998	AU 5820498 A	18-08-1998
WO 9820131 A	14-05-1998	US 5925748 A	20-07-1999
		US 5885776 A	23-03-1999
		AU 5436498 A	29-05-1998
		EP 0942975 A	22-09-1999

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